ADS 503: Cervical Cancer Biopsy Prediction Project

Ruddy Simonpour & Shailja Somani

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```
# load necessary packages for files above
library(Hmisc)
```

```
##
## Attaching package: 'Hmisc'

## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:Hmisc':
##
##     src, summarize

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(pROC)
```

```
## Type 'citation("pROC")' for a citation.

##
## Attaching package: 'pROC'

## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```
library(reshape2)
library(ggplot2)
library(caret)
```

```
## Loading required package: lattice
```

```
library(ROSE)
```

```
## Loaded ROSE 0.0-4
```

```
suppressWarnings({

#setwd("/Users/shailjasomani/Documents/USD_MS_ADS/ADS_503/Final_Proj")   #choose a location/path and se


setwd("/Users/ruddysimonpour/Desktop/University of Sandiego - Curriculum/ADS 503 - Applied Predictive M

source ("Data_Ingestion.R")
source ("Viz_EDA.R")
source ("Preprocessing.R")
source ("Modeling.R")

})
```

```
## Loading required package: colorspace
```

```
##
## Attaching package: 'colorspace'
```

```
## The following object is masked from 'package:pROC':
##
##     coords
```

```
## Loading required package: grid
```

```
## The legacy packages maptools, rgdal, and rgeos, underpinning this package
## will retire shortly. Please refer to R-spatial evolution reports on
## https://r-spatial.org/r/2023/05/15/evolution4.html for details.
## This package is now running under evolution status 0
```

```
## VIM is ready to use.
```

```
## Suggestions and bug-reports can be submitted at: https://github.com/statistikat/VIM/issues
```

```
##
## Attaching package: 'VIM'
```

```
## The following object is masked from 'package:datasets':
##
##     sleep
```

Data Importing

```
# Uses functions from files loaded in to clean data
set.seed(007)

# loading Data
cervical_data_raw <- read_data(x="/Users/ruddysimonpour/Desktop/University of Sandiego - Curriculum/ADS
```

```
## Rows: 858
## Columns: 36
## $ Age                                 <int> 18, 15, 34, 52, 46, 42, 51, 26, 45,~
## $ Number.of.sexual.partners           <dbl> 4, 1, 1, 5, 3, 3, 3, 1, 1, 3, 3, 1,~
## $ First.sexual.intercourse            <dbl> 15, 14, NA, 16, 21, 23, 17, 26, 20,~
## $ Num.of.pregnancies                  <dbl> 1, 1, 1, 4, 4, 2, 6, 3, 5, NA, 4, 3~
## $ Smokes                              <dbl> 0, 0, 0, 1, 0, 0, 1, 0, 0, 1, 0, 0,~
## $ Smokes..years.                      <dbl> 0.000000, 0.000000, 0.000000, 37.00~
## $ Smokes..packs.year.                 <dbl> 0.0, 0.0, 0.0, 37.0, 0.0, 0.0, 3.4,~
## $ Hormonal.Contraceptives             <dbl> 0, 0, 0, 1, 1, 0, 0, 1, 0, 0, 1, 1,~
## $ Hormonal.Contraceptives..years.     <dbl> 0.00, 0.00, 0.00, 3.00, 15.00, 0.00~
## $ IUD                                 <dbl> 0, 0, 0, 0, 0, 0, 1, 1, 0, NA, 0, 0~
## $ IUD..years.                         <dbl> 0, 0, 0, 0, 0, 0, 7, 7, 0, NA, 0, 0~
## $ STDs                                <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs..number.                       <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs.condylomatosis                 <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs.cervical.condylomatosis        <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs.vaginal.condylomatosis         <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs.vulvo.perineal.condylomatosis <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs.syphilis                       <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs.pelvic.inflammatory.disease    <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs.genital.herpes                 <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs.molluscum.contagiosum          <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs.AIDS                           <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs.HIV                            <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs.Hepatitis.B                    <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs.HPV                            <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs..Number.of.diagnosis           <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ STDs..Time.since.first.diagnosis    <dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA,~
## $ STDs..Time.since.last.diagnosis     <dbl> NA, NA, NA, NA, NA, NA, NA, NA, NA,~
## $ Dx.Cancer                           <int> 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0,~
## $ Dx.CIN                              <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ Dx.HPV                              <int> 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0,~
## $ Dx                                  <int> 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0,~
## $ Hinselmann                          <int> 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0,~
## $ Schiller                            <int> 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0,~
## $ Citology                            <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,~
## $ Biopsy                              <int> 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0,~
```

```
#cervical_data_raw <- read_data(x='/Users/shailjasomani/Documents/USD_MS_ADS/ADS_503/Final_Proj/kag_ris
head(cervical_data_raw,5)
```

```
##   Age Number.of.sexual.partners First.sexual.intercourse Num.of.pregnancies
## 1  18                          4                        15                  1
```

```
## 2  15                          1                          14                  1
## 3  34                          1                          NA                  1
## 4  52                          5                          16                  4
## 5  46                          3                          21                  4
##   Smokes Smokes..years. Smokes..packs.year. Hormonal.Contraceptives
## 1      0              0                   0                       0
## 2      0              0                   0                       0
## 3      0              0                   0                       0
## 4      1             37                  37                       1
## 5      0              0                   0                       1
##   Hormonal.Contraceptives..years. IUD IUD..years. STDs STDs..number.
## 1                               0   0           0    0             0
## 2                               0   0           0    0             0
## 3                               0   0           0    0             0
## 4                               3   0           0    0             0
## 5                              15   0           0    0             0
##   STDs.condylomatosis STDs.cervical.condylomatosis STDs.vaginal.condylomatosis
## 1                   0                            0                          0
## 2                   0                            0                          0
## 3                   0                            0                          0
## 4                   0                            0                          0
## 5                   0                            0                          0
##   STDs.vulvo.perineal.condylomatosis STDs.syphilis
## 1                                  0             0
## 2                                  0             0
## 3                                  0             0
## 4                                  0             0
## 5                                  0             0
##   STDs.pelvic.inflammatory.disease STDs.genital.herpes
## 1                                0                   0
## 2                                0                   0
## 3                                0                   0
## 4                                0                   0
## 5                                0                   0
##   STDs.molluscum.contagiosum STDs.AIDS STDs.HIV STDs.Hepatitis.B STDs.HPV
## 1                          0         0        0                0        0
## 2                          0         0        0                0        0
## 3                          0         0        0                0        0
## 4                          0         0        0                0        0
## 5                          0         0        0                0        0
##   STDs..Number.of.diagnosis STDs..Time.since.first.diagnosis
## 1                         0                              NA
## 2                         0                              NA
## 3                         0                              NA
## 4                         0                              NA
## 5                         0                              NA
##   STDs..Time.since.last.diagnosis Dx.Cancer Dx.CIN Dx.HPV Dx Hinselmann
## 1                              NA         0      0      0  0          0
## 2                              NA         0      0      0  0          0
## 3                              NA         0      0      0  0          0
## 4                              NA         1      0      1  0          0
## 5                              NA         0      0      0  0          0
##   Schiller Citology Biopsy
## 1        0        0      0
```

```
## 2        0        0      0
## 3        0        0      0
## 4        0        0      0
## 5        0        0      0
```

```
dim(cervical_data_raw)
```

```
## [1] 858  36
```

```
# check missing data
null_counts_raw <- check_nulls(cervical_data_raw)
```

```
##                                                                  Column
## Age                                                                 Age
## Number.of.sexual.partners                     Number.of.sexual.partners
## First.sexual.intercourse                       First.sexual.intercourse
## Num.of.pregnancies                                 Num.of.pregnancies
## Smokes                                                         Smokes
## Smokes..years.                                         Smokes..years.
## Smokes..packs.year.                                 Smokes..packs.year.
## Hormonal.Contraceptives                       Hormonal.Contraceptives
## Hormonal.Contraceptives..years.       Hormonal.Contraceptives..years.
## IUD                                                               IUD
## IUD..years.                                               IUD..years.
## STDs                                                             STDs
## STDs..number.                                           STDs..number.
## STDs.condylomatosis                               STDs.condylomatosis
## STDs.cervical.condylomatosis             STDs.cervical.condylomatosis
## STDs.vaginal.condylomatosis               STDs.vaginal.condylomatosis
## STDs.vulvo.perineal.condylomatosis STDs.vulvo.perineal.condylomatosis
## STDs.syphilis                                       STDs.syphilis
## STDs.pelvic.inflammatory.disease     STDs.pelvic.inflammatory.disease
## STDs.genital.herpes                               STDs.genital.herpes
## STDs.molluscum.contagiosum                 STDs.molluscum.contagiosum
## STDs.AIDS                                                   STDs.AIDS
## STDs.HIV                                                     STDs.HIV
## STDs.Hepatitis.B                                     STDs.Hepatitis.B
## STDs.HPV                                                     STDs.HPV
## STDs..Number.of.diagnosis                   STDs..Number.of.diagnosis
## STDs..Time.since.first.diagnosis     STDs..Time.since.first.diagnosis
## STDs..Time.since.last.diagnosis       STDs..Time.since.last.diagnosis
## Dx.Cancer                                                   Dx.Cancer
## Dx.CIN                                                         Dx.CIN
## Dx.HPV                                                         Dx.HPV
## Dx                                                                 Dx
## Hinselmann                                                 Hinselmann
## Schiller                                                     Schiller
## Citology                                                     Citology
## Biopsy                                                         Biopsy
## 37                                                              Total
##                                          Nulls      ColumnPercentage
## Age                                          0                     0
## Number.of.sexual.partners                   26      3.03030303030303
```

```
## First.sexual.intercourse                     7     0.815850815850816
## Num.of.pregnancies                          56      6.52680652680653
## Smokes                                      13      1.51515151515152
## Smokes..years.                              13      1.51515151515152
## Smokes..packs.year.                         13      1.51515151515152
## Hormonal.Contraceptives                    108      12.5874125874126
## Hormonal.Contraceptives..years.            108      12.5874125874126
## IUD                                        117      13.6363636363636
## IUD..years.                                117      13.6363636363636
## STDs                                       105      12.2377622377622
## STDs..number.                              105      12.2377622377622
## STDs.condylomatosis                        105      12.2377622377622
## STDs.cervical.condylomatosis               105      12.2377622377622
## STDs.vaginal.condylomatosis                105      12.2377622377622
## STDs.vulvo.perineal.condylomatosis         105      12.2377622377622
## STDs.syphilis                              105      12.2377622377622
## STDs.pelvic.inflammatory.disease           105      12.2377622377622
## STDs.genital.herpes                        105      12.2377622377622
## STDs.molluscum.contagiosum                 105      12.2377622377622
## STDs.AIDS                                  105      12.2377622377622
## STDs.HIV                                   105      12.2377622377622
## STDs.Hepatitis.B                           105      12.2377622377622
## STDs.HPV                                   105      12.2377622377622
## STDs..Number.of.diagnosis                    0                     0
## STDs..Time.since.first.diagnosis           787      91.7249417249417
## STDs..Time.since.last.diagnosis            787      91.7249417249417
## Dx.Cancer                                    0                     0
## Dx.CIN                                       0                     0
## Dx.HPV                                       0                     0
## Dx                                           0                     0
## Hinselmann                                   0                     0
## Schiller                                     0                     0
## Citology                                     0                     0
## Biopsy                                       0                     0
## 37                                 total_nulls total_percentage_null
```

```
# remove cols with more than 85% missing data
cervical_data_clean <- remove_cols(cervical_data_raw)
```

```
##                                                                Column
## Age                                                               Age
## Number.of.sexual.partners                  Number.of.sexual.partners
## First.sexual.intercourse                    First.sexual.intercourse
## Num.of.pregnancies                                Num.of.pregnancies
## Smokes                                                       Smokes
## Smokes..years.                                       Smokes..years.
## Smokes..packs.year.                                Smokes..packs.year.
## Hormonal.Contraceptives                        Hormonal.Contraceptives
## Hormonal.Contraceptives..years.      Hormonal.Contraceptives..years.
## IUD                                                              IUD
## IUD..years.                                             IUD..years.
## STDs                                                            STDs
## STDs..number.                                          STDs..number.
## STDs.condylomatosis                                 STDs.condylomatosis
```

```
## STDs.cervical.condylomatosis             STDs.cervical.condylomatosis
## STDs.vaginal.condylomatosis               STDs.vaginal.condylomatosis
## STDs.vulvo.perineal.condylomatosis STDs.vulvo.perineal.condylomatosis
## STDs.syphilis                                         STDs.syphilis
## STDs.pelvic.inflammatory.disease     STDs.pelvic.inflammatory.disease
## STDs.genital.herpes                               STDs.genital.herpes
## STDs.molluscum.contagiosum                 STDs.molluscum.contagiosum
## STDs.AIDS                                               STDs.AIDS
## STDs.HIV                                                 STDs.HIV
## STDs.Hepatitis.B                                 STDs.Hepatitis.B
## STDs.HPV                                                 STDs.HPV
## STDs..Number.of.diagnosis                 STDs..Number.of.diagnosis
## STDs..Time.since.first.diagnosis     STDs..Time.since.first.diagnosis
## STDs..Time.since.last.diagnosis       STDs..Time.since.last.diagnosis
## Dx.Cancer                                               Dx.Cancer
## Dx.CIN                                                     Dx.CIN
## Dx.HPV                                                     Dx.HPV
## Dx                                                             Dx
## Hinselmann                                             Hinselmann
## Schiller                                                 Schiller
## Citology                                                 Citology
## Biopsy                                                     Biopsy
## 37                                                          Total
##                                        Nulls      ColumnPercentage
## Age                                        0                     0
## Number.of.sexual.partners                 26      3.03030303030303
## First.sexual.intercourse                   7     0.815850815850816
## Num.of.pregnancies                        56      6.52680652680653
## Smokes                                    13      1.51515151515152
## Smokes..years.                            13      1.51515151515152
## Smokes..packs.year.                       13      1.51515151515152
## Hormonal.Contraceptives                  108      12.5874125874126
## Hormonal.Contraceptives..years.          108      12.5874125874126
## IUD                                      117      13.6363636363636
## IUD..years.                              117      13.6363636363636
## STDs                                     105      12.2377622377622
## STDs..number.                            105      12.2377622377622
## STDs.condylomatosis                      105      12.2377622377622
## STDs.cervical.condylomatosis             105      12.2377622377622
## STDs.vaginal.condylomatosis              105      12.2377622377622
## STDs.vulvo.perineal.condylomatosis       105      12.2377622377622
## STDs.syphilis                            105      12.2377622377622
## STDs.pelvic.inflammatory.disease         105      12.2377622377622
## STDs.genital.herpes                      105      12.2377622377622
## STDs.molluscum.contagiosum               105      12.2377622377622
## STDs.AIDS                                105      12.2377622377622
## STDs.HIV                                 105      12.2377622377622
## STDs.Hepatitis.B                         105      12.2377622377622
## STDs.HPV                                 105      12.2377622377622
## STDs..Number.of.diagnosis                  0                     0
## STDs..Time.since.first.diagnosis         787      91.7249417249417
## STDs..Time.since.last.diagnosis          787      91.7249417249417
## Dx.Cancer                                  0                     0
## Dx.CIN                                     0                     0
```

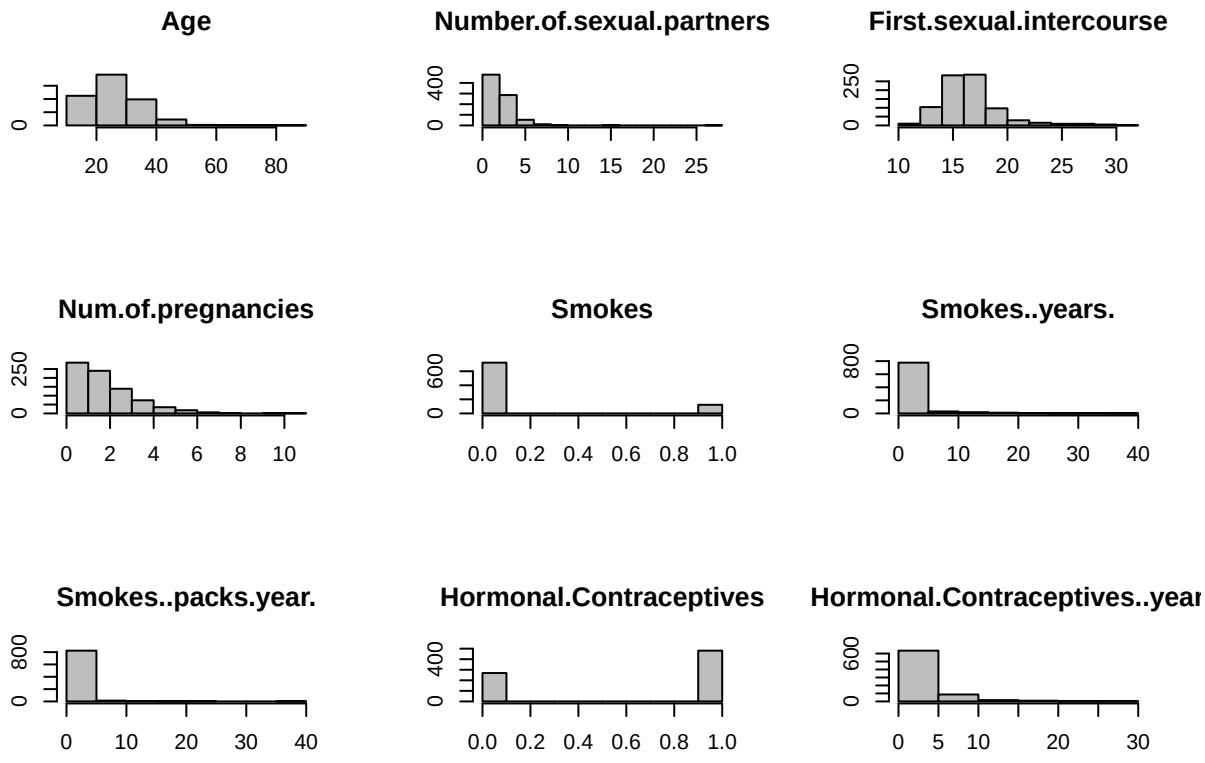
```
## Dx.HPV                                0                    0
## Dx                                    0                    0
## Hinselmann                            0                    0
## Schiller                              0                    0
## Citology                              0                    0
## Biopsy                                0                    0
## 37                        total_nulls total_percentage_null
```

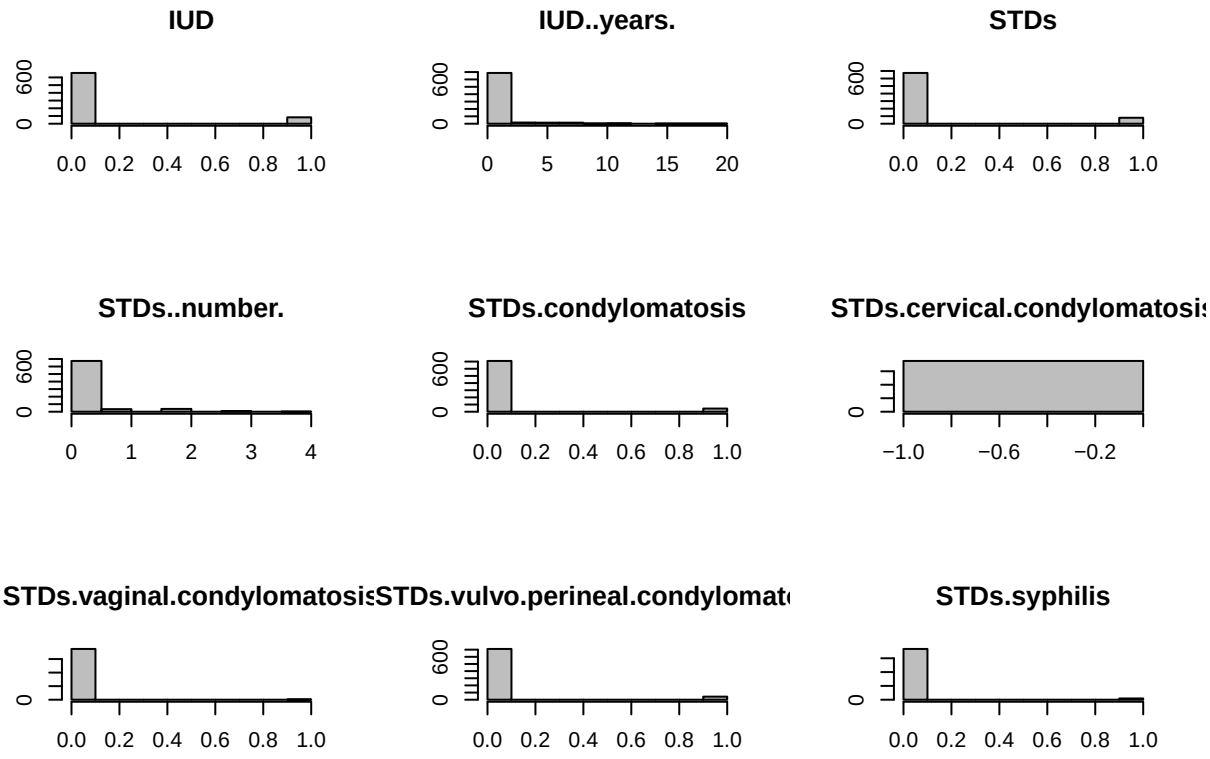
```
dim(cervical_data_clean)
```

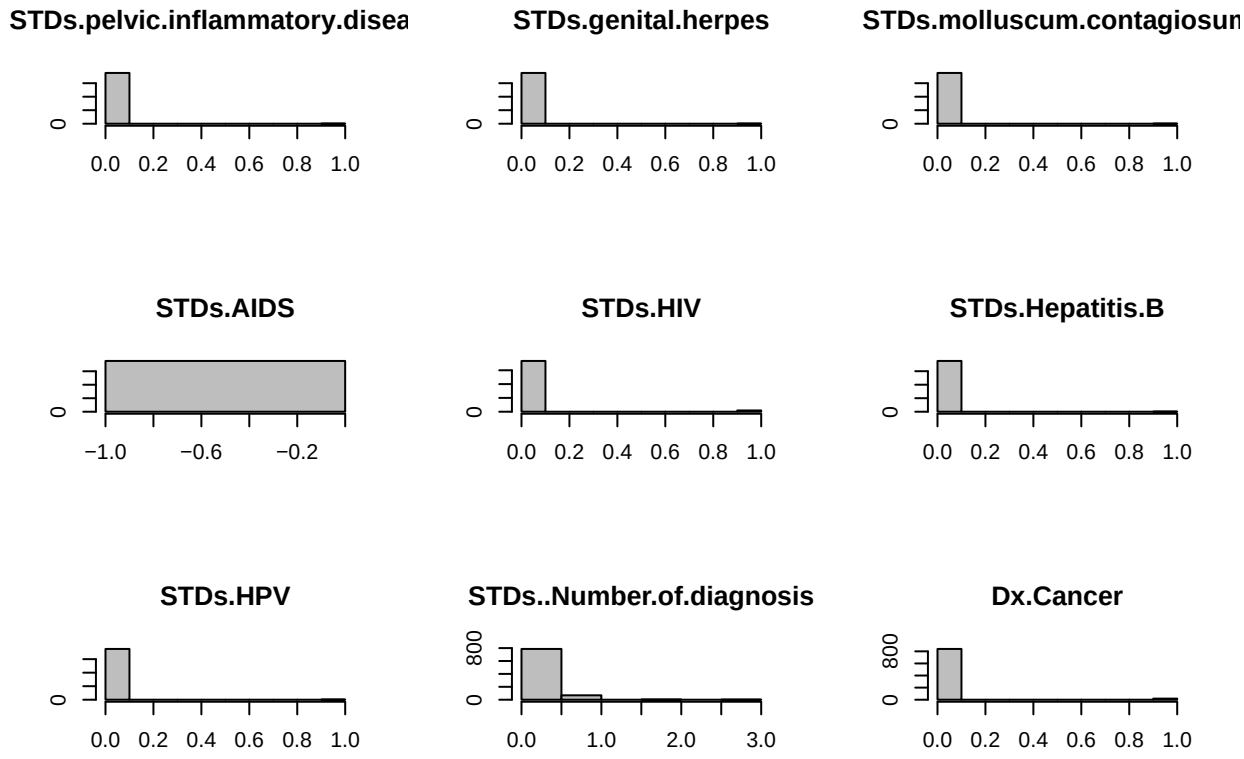
```
## [1] 858  34
```

EDA Analysis

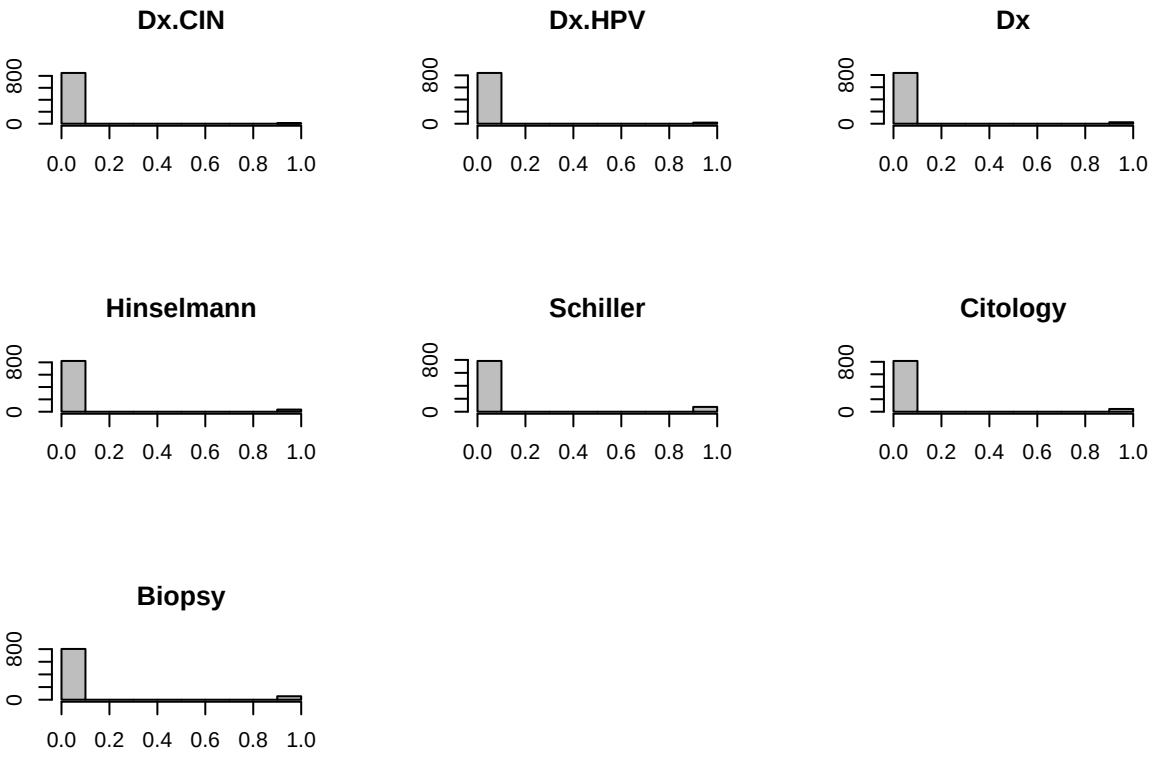
```
# These user-defined functions are pulled from the Viz_EDA.R file.
# Look at all histograms of features collectively
hist.df(cervical_data_clean)
```

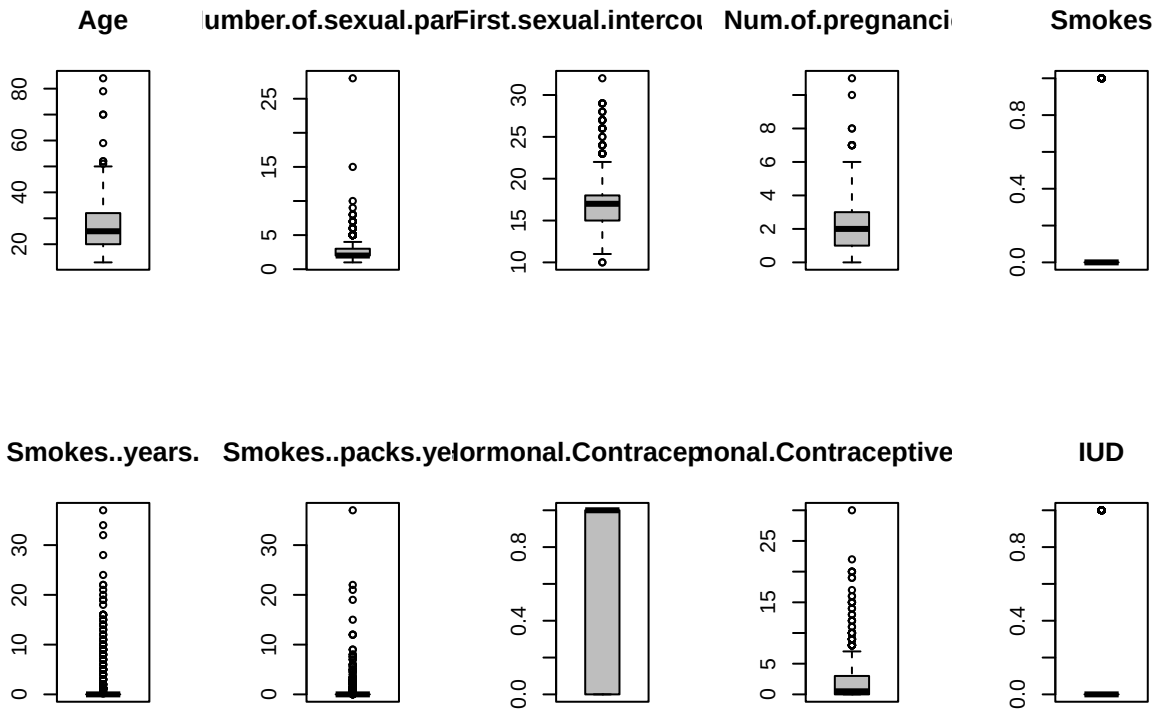


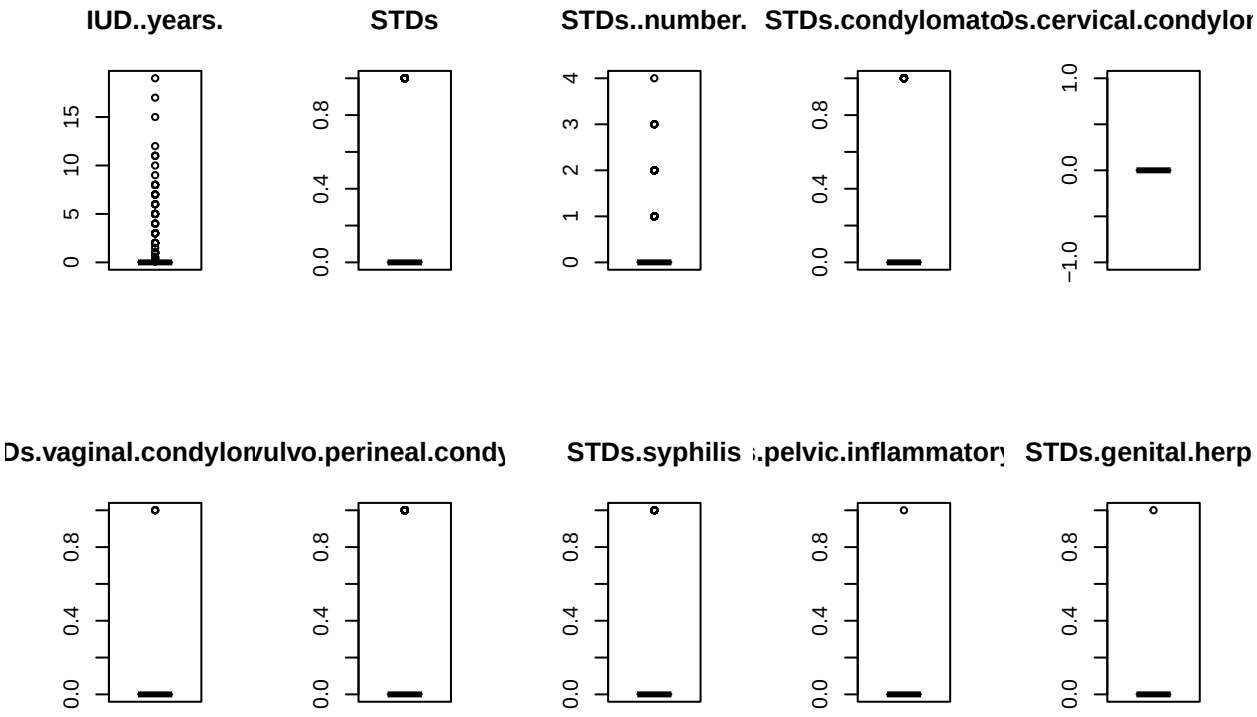

IUD
0 600
0.0 0.2 0.4 0.6 0.8 1.0
IUD..years.
0 600
0 5 10 15 20
STDs
0 600
0.0 0.2 0.4 0.6 0.8 1.0
STDs..number.
0 600
0 1 2 3 4
STDs.condylomatosis
0 600
0.0 0.2 0.4 0.6 0.8 1.0
STDs.cervical.condylomatosis
0
−1.0 −0.6 −0.2
STDs.vaginal.condylomatosis
0
0.0 0.2 0.4 0.6 0.8 1.0
STDs.vulvo.perineal.condylomat
0 600
0.0 0.2 0.4 0.6 0.8 1.0
STDs.syphilis
0
0.0 0.2 0.4 0.6 0.8 1.0

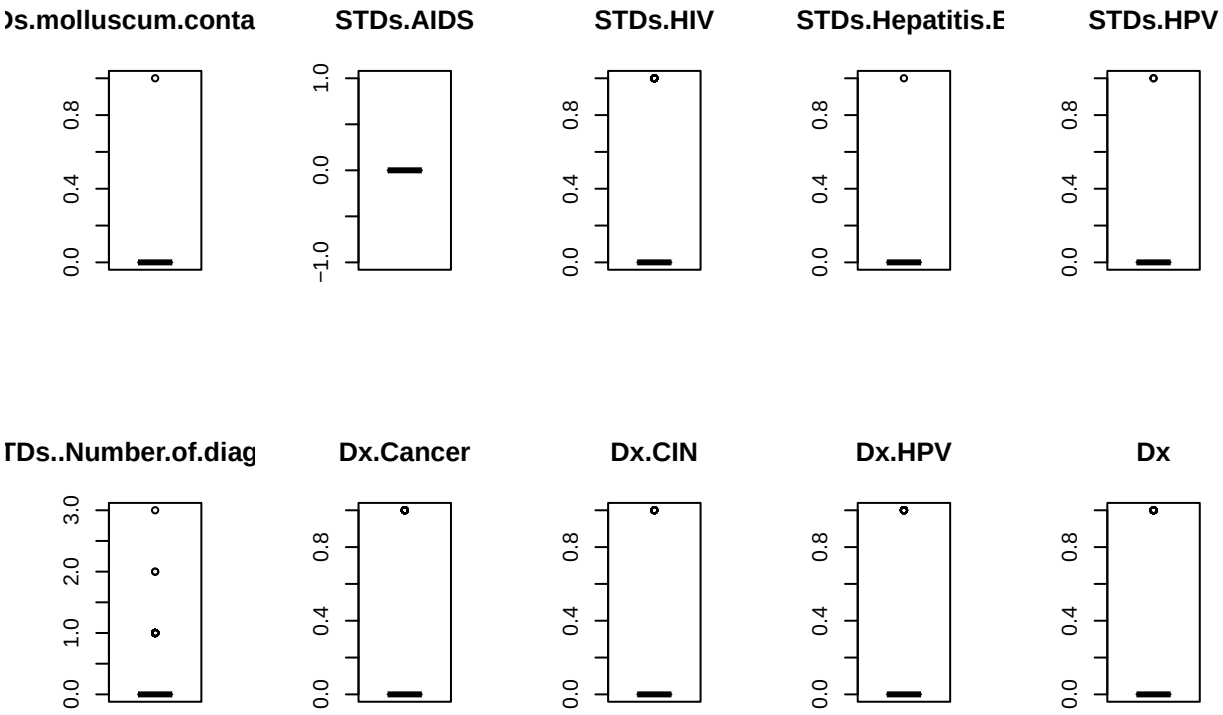


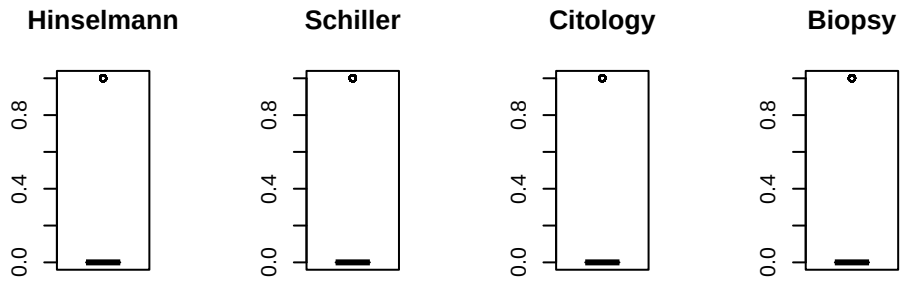

```
# Create boxplots for all features - helps visualize outliers
boxplot.df(cervical_data_clean)
```


Dx.CIN
0
800
0.0 0.2 0.4 0.6 0.8 1.0
Dx.HPV
0
800
0.0 0.2 0.4 0.6 0.8 1.0
Dx
0
800
0.0 0.2 0.4 0.6 0.8 1.0
Hinselmann
0
800
0.0 0.2 0.4 0.6 0.8 1.0
Schiller
0
800
0.0 0.2 0.4 0.6 0.8 1.0
Citology
0
800
0.0 0.2 0.4 0.6 0.8 1.0
Biopsy
0
800
0.0 0.2 0.4 0.6 0.8 1.0


Age
umber.of.sexual.par
First.sexual.interco
Num.of.pregnanci
Smokes
Smokes..years.
Smokes..packs.ye
ormonal.Contracep
nal.Contraceptive
IUD


IUD..years.
STDs
STDs..number.
STDs.condylomato
Ds.cervical.condylor
0 5 10 15
0.0 0.4 0.8
0 1 2 3 4
0.0 0.4 0.8
−1.0 0.0 1.0
Ds.vaginal.condylor
vulvo.perineal.condy
STDs.syphilis
.pelvic.inflammator
STDs.genital.herp
0.0 0.4 0.8
0.0 0.4 0.8
0.0 0.4 0.8
0.0 0.4 0.8
0.0 0.4 0.8


Os.molluscum.conta
STDs.AIDS
STDs.HIV
STDs.Hepatitis.E
STDs.HPV
0.0
0.4
0.8
−1.0
0.0
1.0
0.0
1.0
2.0
3.0
TDs..Number.of.diag
Dx.Cancer
Dx.CIN
Dx.HPV
Dx



Data Cleaning

```
library(caret)

# remove near zero variance variables
dim(cervical_data_clean)
```

```
## [1] 858  34
```

```
degeneratecols <- nearZeroVar(cervical_data_clean)

length(degeneratecols) # number of cols that are degenerate distributions
```

```
## [1] 18
```

```
cervical_data_process <- cervical_data_clean[, -degeneratecols]
dim(cervical_data_process)
```

```
## [1] 858  16
```

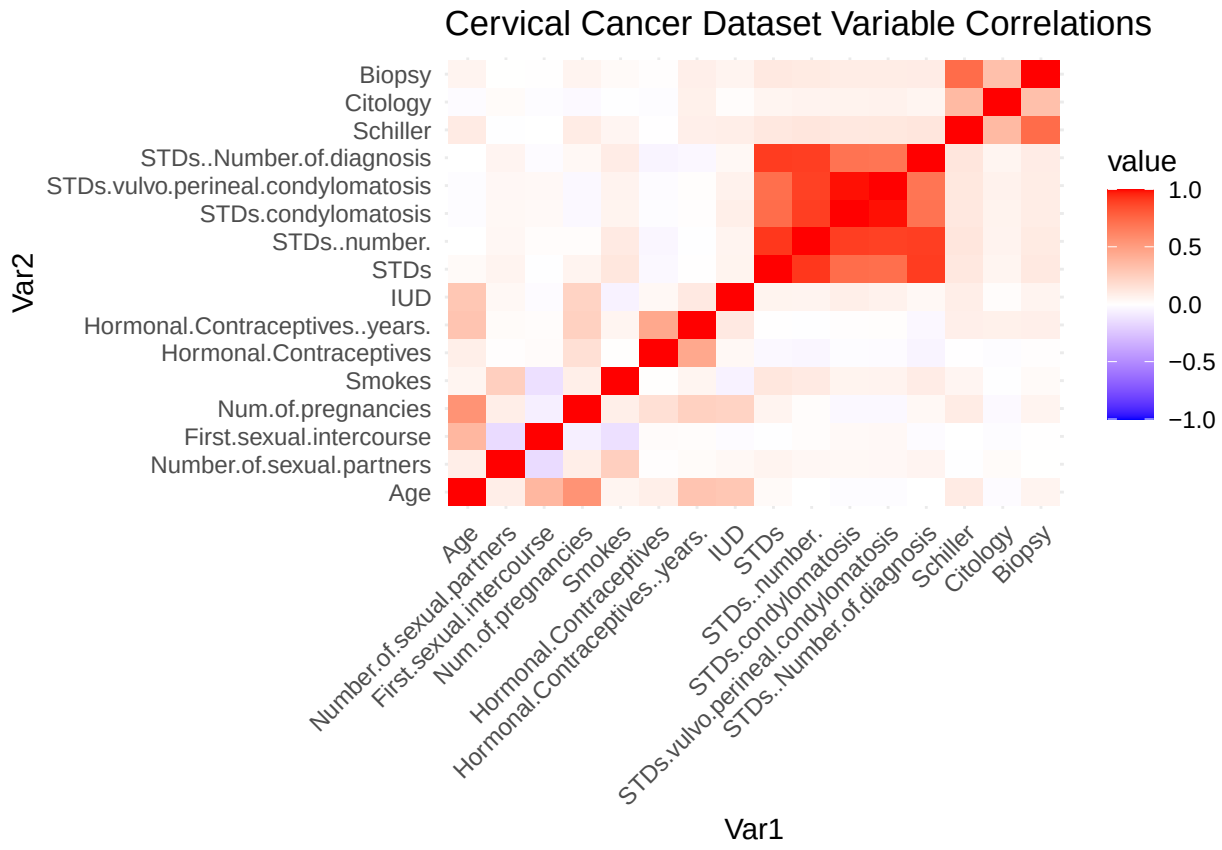
```r
# impute missing values with knn
#data_clean <- impute_with_knn(cervical_data_process, k = 29) # the rule of thumbs choosing the k is th
preproc <- preProcess(cervical_data_process, method = ("knnImpute"))
data_clean <- predict(preproc, cervical_data_process)

# since knn imputation create new columns, we will exclude the new columns from our dataset
data_clean <- subset(data_clean, select = Age:Biopsy)

null_counts_clean <- check_nulls(data_clean)
```

```
##                                                                  Column
## Age                                                                 Age
## Number.of.sexual.partners                     Number.of.sexual.partners
## First.sexual.intercourse                       First.sexual.intercourse
## Num.of.pregnancies                                   Num.of.pregnancies
## Smokes                                                           Smokes
## Hormonal.Contraceptives                         Hormonal.Contraceptives
## Hormonal.Contraceptives..years.       Hormonal.Contraceptives..years.
## IUD                                                                 IUD
## STDs                                                               STDs
## STDs..number.                                             STDs..number.
## STDs.condylomatosis                                 STDs.condylomatosis
## STDs.vulvo.perineal.condylomatosis STDs.vulvo.perineal.condylomatosis
## STDs..Number.of.diagnosis                     STDs..Number.of.diagnosis
## Schiller                                                       Schiller
## Citology                                                       Citology
## Biopsy                                                           Biopsy
## 17                                                                Total
##                                        Nulls      ColumnPercentage
## Age                                        0                     0
## Number.of.sexual.partners                  0                     0
## First.sexual.intercourse                   0                     0
## Num.of.pregnancies                         0                     0
## Smokes                                     0                     0
## Hormonal.Contraceptives                    0                     0
## Hormonal.Contraceptives..years.            0                     0
## IUD                                        0                     0
## STDs                                       0                     0
## STDs..number.                              0                     0
## STDs.condylomatosis                        0                     0
## STDs.vulvo.perineal.condylomatosis         0                     0
## STDs..Number.of.diagnosis                  0                     0
## Schiller                                   0                     0
## Citology                                   0                     0
## Biopsy                                     0                     0
## 17                                total_nulls total_percentage_null
```

EDA - Correlations Analysis

```r
# convert factor to numeric
data_clean$Biopsy <- as.numeric(data_clean$Biopsy)
```

```
# Feed into our heatmap function
heatmap <- create_heatmap("Cervical Cancer Dataset Variable Correlations", data_clean)

# Display the heatmap
print(heatmap)
```




```
ggsave(filename = "cor-matrix.png", plot = heatmap, width = 7, height = 7)
```

Check highly correlated predictors

```
highlyCorrelated <- findCorrelation(cor(data_clean), cutoff = 0.9)

print(names(data_clean)[highlyCorrelated])
```

```
## [1] "STDs..number."       "STDs"                "STDs.condylomatosis"
```

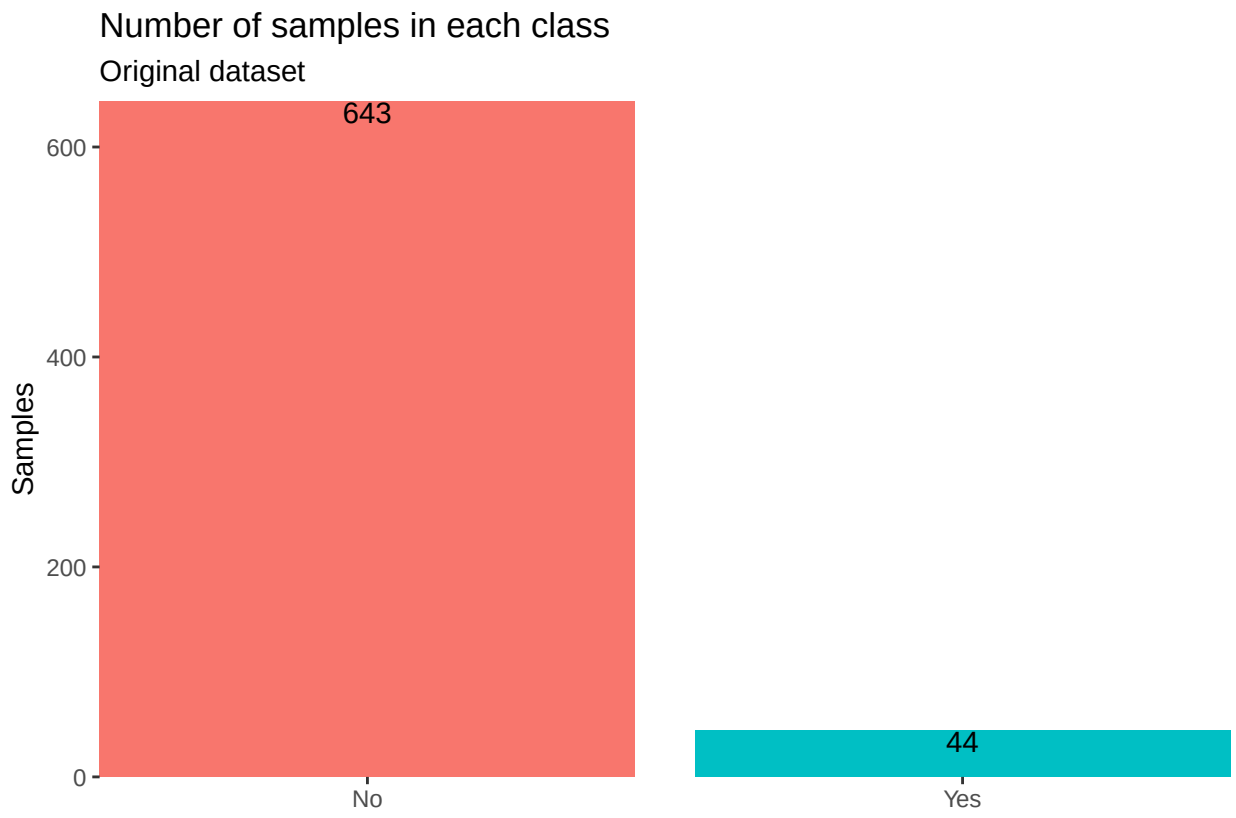
```
# drop highly correlated variables
data_clean <- data_clean[, -highlyCorrelated]
```

Convert the class to factor variable

```
# initial look at the target variable
data_clean$Biopsy<-as.factor(data_clean$Biopsy) # convert class to factor
levels(data_clean$Biopsy) <- c("No", "Yes") # names of the factors
```

Data Partitioning (Train and Test Split)

```
# data splitting
set.seed(100)

trainIndex <- createDataPartition(data_clean$Biopsy, p = .8, list = FALSE)
trainData <- data_clean[trainIndex, ]
testData  <- data_clean[-trainIndex, ]

train_X <- trainData[ , !(names(trainData) %in% "Biopsy")]
train_y <- trainData$Biopsy

test_X <- testData[ , !(names(testData) %in% "Biopsy")]
test_y <- testData$Biopsy


############################################### Imbalance class

# plotting number of samples in each class - original dataset
options(scipen=10000)

train_y_df <- data.frame(Biopsy = train_y)

# Create the plot
p <- ggplot(data = train_y_df, aes(x = Biopsy, fill = Biopsy)) +
    geom_bar() +
    geom_text(stat='count', aes(label=..count..), vjust=1) +
    ggtitle("Number of samples in each class", subtitle = "Original dataset") +
    xlab("") +
    ylab("Samples") +
    scale_y_continuous(expand = c(0,0)) +
    scale_x_discrete(expand = c(0,0)) +
    theme(legend.position = "none",
          legend.title = element_blank(),
          panel.grid.major = element_blank(),
          panel.grid.minor = element_blank(),
          panel.background = element_blank())
p
```

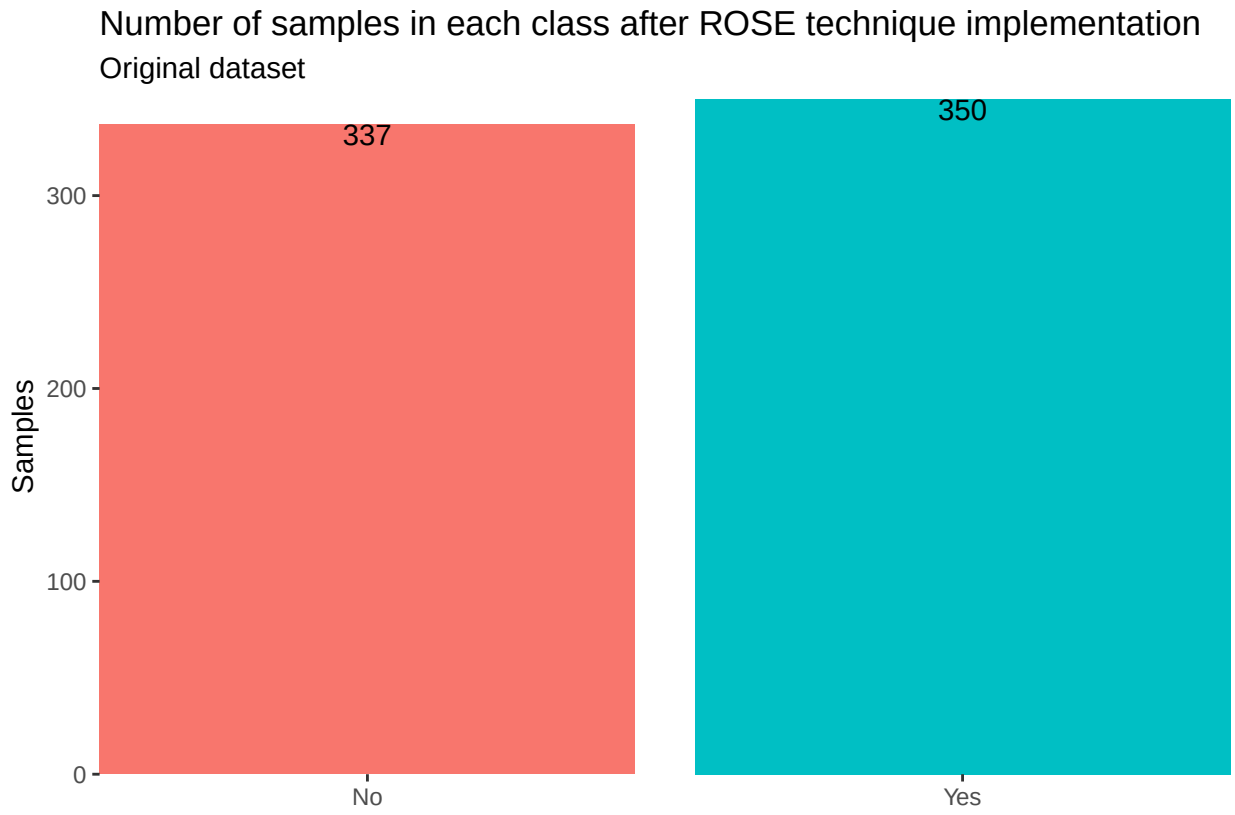



```
ggsave(filename = "class_imbalance1.png", plot = p, width = 7, height = 7)
```

Class Imbalanace (ROSE)

```
#Implementing ROSE function to handle class imbalance problem

library(ROSE)

set.seed(100)

rose_train <- ROSE(Biopsy ~ ., data = trainData)$data

train_X <- rose_train[ , !(names(rose_train) %in% "Biopsy")]
train_y <- rose_train$Biopsy


options(scipen=10000)

train_y_df <- data.frame(Biopsy = train_y)

p1 <- ggplot(data = train_y_df, aes(x = Biopsy,fill = Biopsy)) +
    geom_bar()+
    geom_text(stat='count', aes(label=..count..), vjust=1) +
    ggtitle("Number of samples in each class after ROSE technique implementation", subtitle = "Original
```

```
    xlab("")+
    ylab("Samples")+
    scale_y_continuous(expand = c(0,0))+
    scale_x_discrete(expand = c(0,0))+
    theme(legend.position = "none",
          legend.title = element_blank(),
          panel.grid.major = element_blank(),
          panel.grid.minor = element_blank(),
          panel.background = element_blank())
p1
```




```
ggsave(filename = "class_imbalance2.png", plot = p1, width = 7, height = 4)
```

Data Pre-Processing

```
preProcValues <- preProcess(train_X,
                            method = c("center", "scale"))

train_X <- predict(preProcValues, train_X)
test_X <- predict(preProcValues, test_X)


cntrl <- trainControl(method = "cv", number = 10,
```

```
                    summaryFunction = twoClassSummary,
                    classProbs = TRUE,
                    savePredictions = TRUE)
```

Modeling

Non-Linear models

Neural Network Model

```
### Neural Network Model
nnet_model <- train_nnet_model(train_X, train_y, ncol(trainData), cntrl)
```

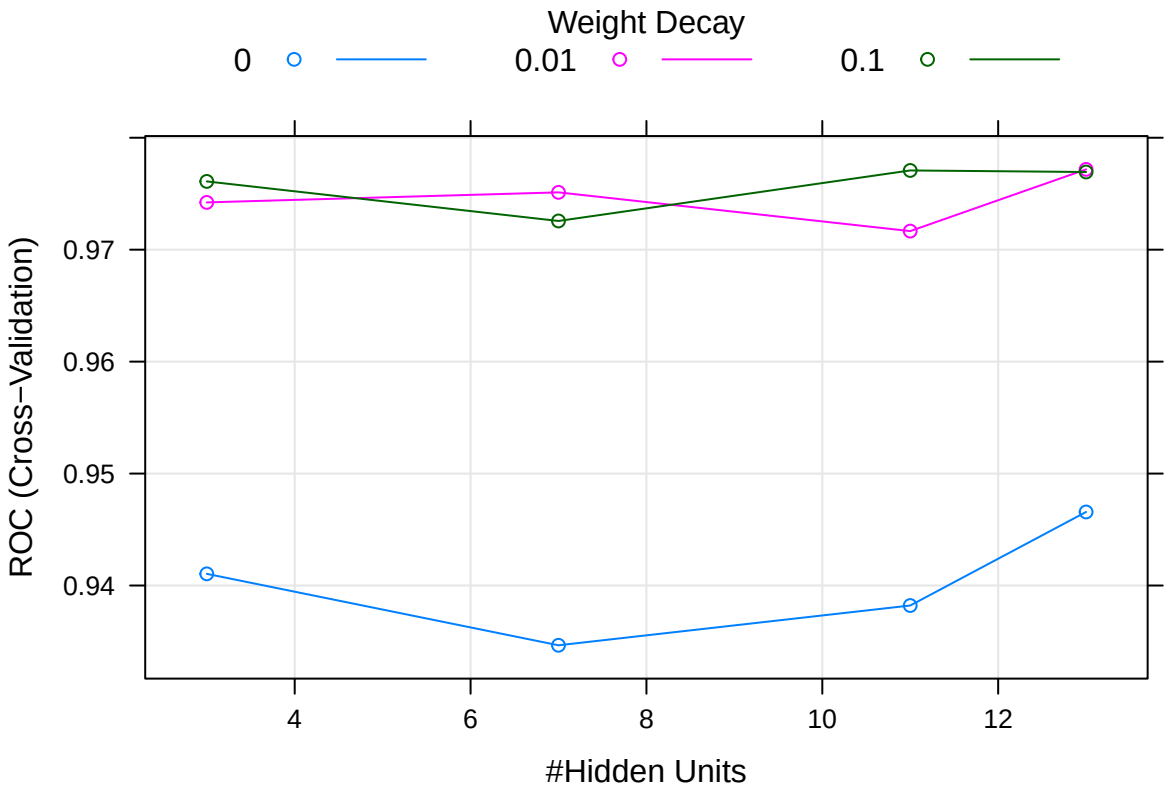
```
## Warning in train.default(x = train_X, y = train_y, method = "nnet", tuneGrid =
## nnetGrid, : The metric "Accuracy" was not in the result set. ROC will be used
## instead.
```

```
# get prediction result
testResults_nnet <- get_prediction_results(nnet_model, test_X, test_y)

# convert prediction levels to match observation
testResults_nnet$prediction <- ifelse(testResults_nnet$prediction == "1", "Yes", "No")

# confusion matrix
cm <- confusionMatrix(as.factor(testResults_nnet$prediction), as.factor(testResults_nnet$observation))
print(cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  151   3
##        Yes   9   8
##
##                Accuracy : 0.9298
##                  95% CI : (0.8806, 0.9632)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 0.6924
##
##                   Kappa : 0.5351
##
##  Mcnemar's Test P-Value : 0.1489
##
##             Sensitivity : 0.9437
##             Specificity : 0.7273
##          Pos Pred Value : 0.9805
##          Neg Pred Value : 0.4706
##              Prevalence : 0.9357
##          Detection Rate : 0.8830
```

```
##    Detection Prevalence : 0.9006
##       Balanced Accuracy : 0.8355
##
##        'Positive' Class : No
##
```

```
# neural network model result plot
plot(nnet_model)
```




```
nnet_model$finalModel
```

```
## a 12-13-1 network with 183 weights
## inputs: Age Number.of.sexual.partners First.sexual.intercourse Num.of.pregnancies Smokes Hormonal.Co
## output(s): .outcome
## options were - entropy fitting  decay=0.01
```

```
# roc/auc result
roc_nnet <- roc(testResults_nnet$observation, testResults_nnet$class_prob)
```

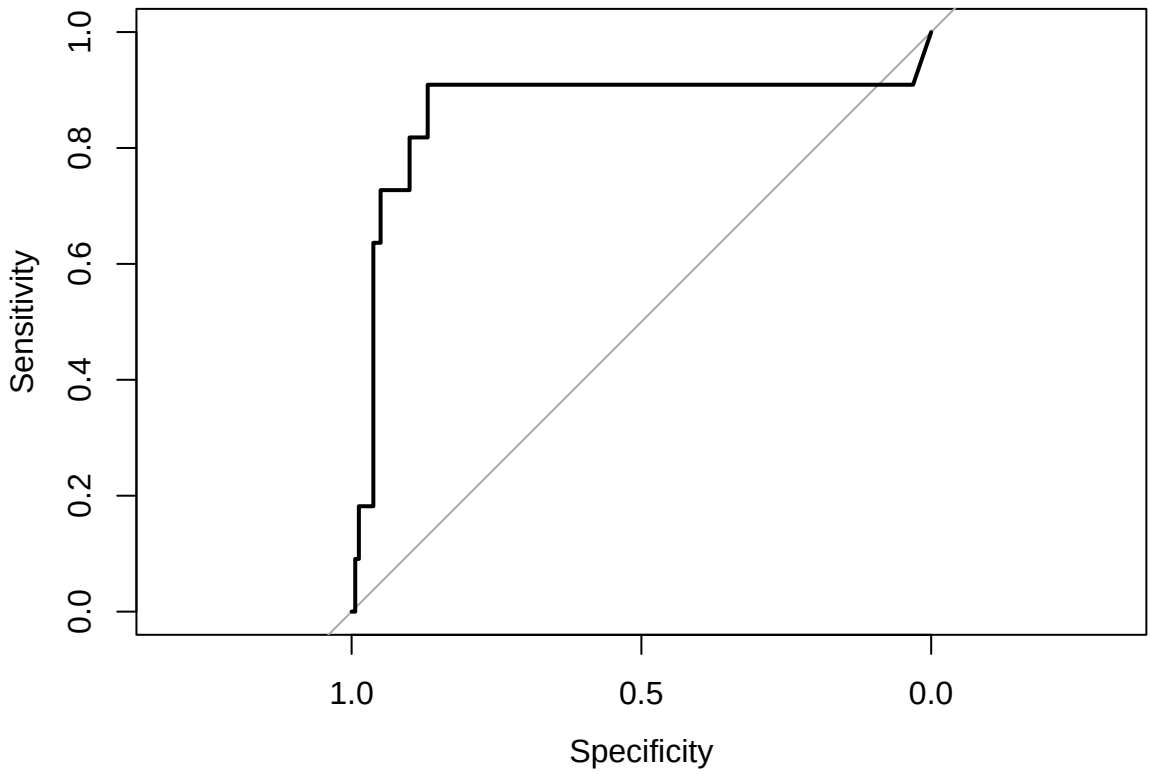
```
## Setting levels: control = No, case = Yes
```

```
## Setting direction: controls < cases
```

```
auc(roc_nnet)
```

```
## Area under the curve: 0.8662
```

```
plot(roc_nnet)
```



Multivariate Adaptive Regression Splines (MARS)

```
mars_model <- train_mars_model(train_X, train_y, 2:20, cntrl)
```

```
## Warning in train.default(x = train_X, y = train_y, method = "earth", tuneGrid =
## expand.grid(degree = 1, : The metric "Accuracy" was not in the result set. ROC
## will be used instead.
```

```
## Loading required package: earth
```

```
## Loading required package: Formula
```

```
## Loading required package: plotmo
```

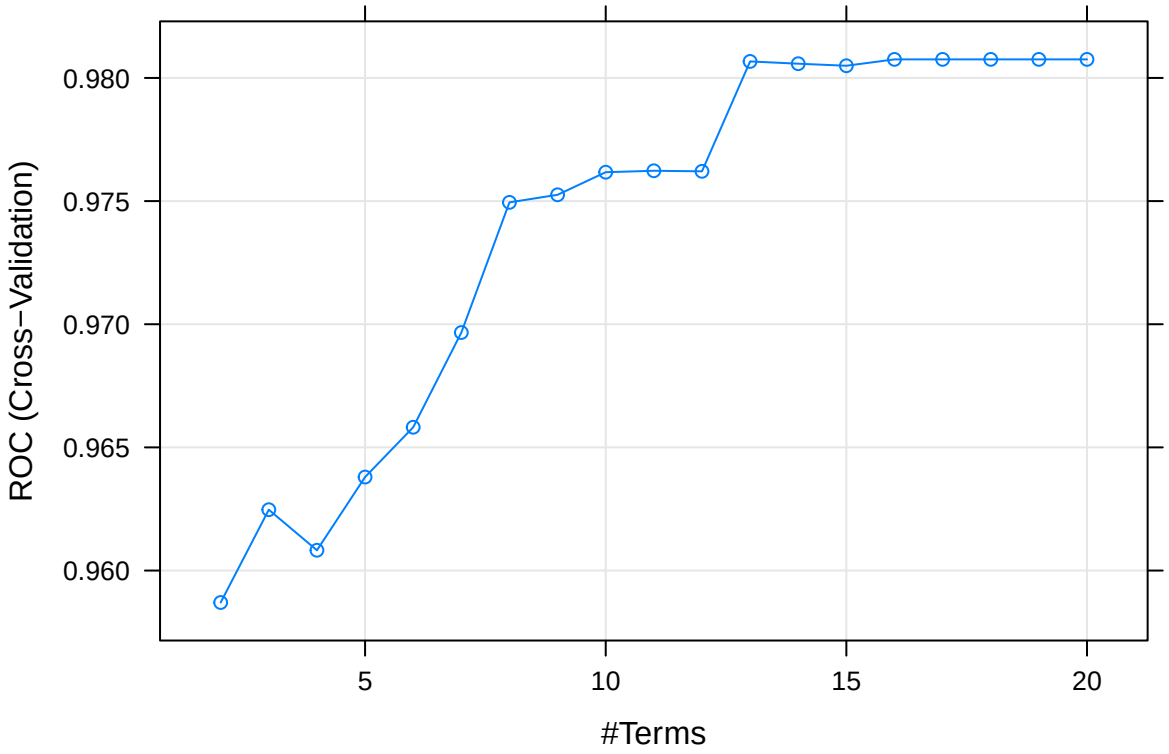
```
## Loading required package: plotrix
```

```
## Loading required package: TeachingDemos

##
## Attaching package: 'TeachingDemos'

## The following objects are masked from 'package:Hmisc':
##
##     cnvrt.coords, subplot

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```r
# get prediction result
testResults_mars <- get_prediction_results(mars_model, test_X, test_y)

# convert prediction levels to match observation
testResults_mars$prediction <- ifelse(testResults_mars$prediction == "1", "Yes", "No")

# confusion matrix
cm <- confusionMatrix(as.factor(testResults_mars$prediction), as.factor(testResults_mars$observation))
print(cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  151   3
##        Yes   9   8
##
##                Accuracy : 0.9298
##                  95% CI : (0.8806, 0.9632)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 0.6924
##
##                   Kappa : 0.5351
##
##  Mcnemar's Test P-Value : 0.1489
##
##             Sensitivity : 0.9437
##             Specificity : 0.7273
##          Pos Pred Value : 0.9805
##          Neg Pred Value : 0.4706
##              Prevalence : 0.9357
##          Detection Rate : 0.8830
##    Detection Prevalence : 0.9006
##       Balanced Accuracy : 0.8355
##
##        'Positive' Class : No
##
```

```r
# mars model result plot
plot(mars_model)
```




```
mars_model$finalModel
```

```
## GLM (family binomial, link logit):
##  nulldev  df       dev  df   devratio     AIC iters converged
##  952.138 686   118.065 673      0.876   146.1     9         1
##
## Earth selected 14 of 20 terms, and 7 of 12 predictors (nprune=16)
## Termination condition: Reached nk 25
## Importance: Schiller, STDs..Number.of.diagnosis, First.sexual.intercourse, ...
## Number of terms at each degree of interaction: 1 13 (additive model)
## Earth GCV 0.03567786    RSS 22.62195    GRSq 0.8576527    RSq 0.8682384
```

```
# roc/auc result
roc_mars <- roc(testResults_mars$observation, testResults_mars$class_prob)
```

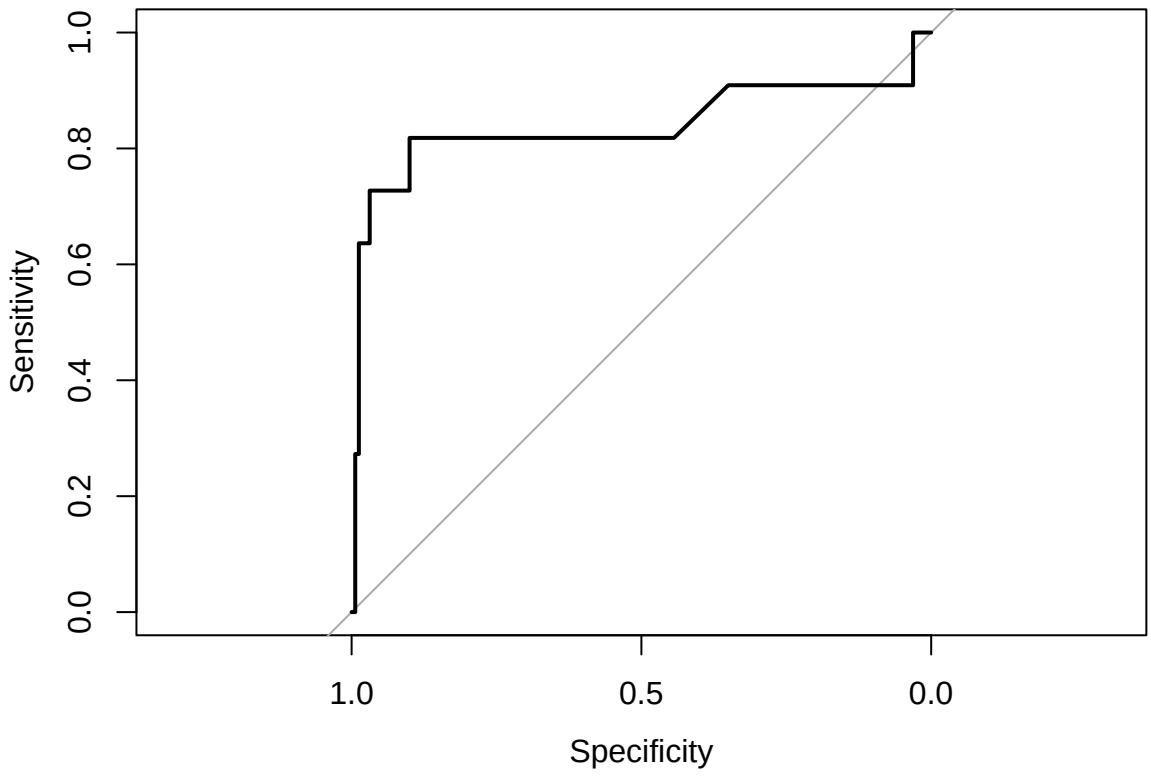
```
## Setting levels: control = No, case = Yes
```

```
## Setting direction: controls < cases
```

```
auc(roc_mars)
```

```
## Area under the curve: 0.8389
```

```
plot(roc_mars)
```



Support Vector Machine (SVM)

```
svm_model <- train_svm_model(train_X, train_y, 20, cntrl)
```

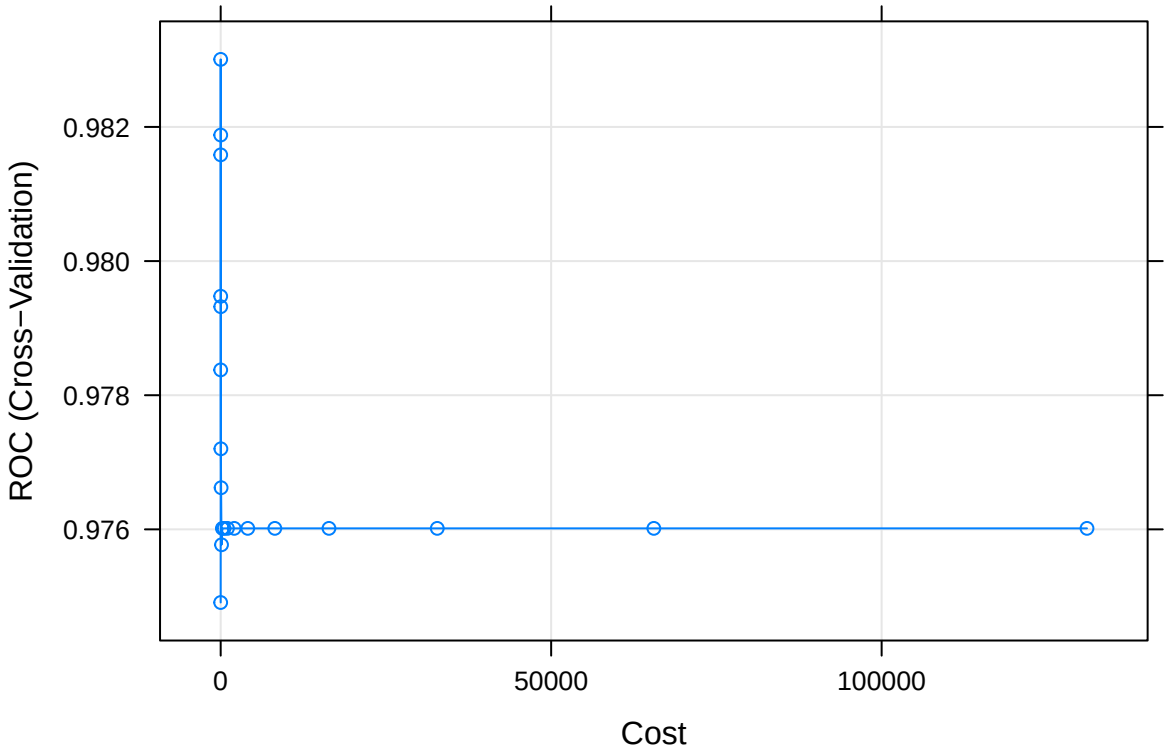
```
# get prediction result
testResults_svm <- get_prediction_results(svm_model, test_X, test_y)

# convert prediction levels to match observation
testResults_svm$prediction <- ifelse(testResults_svm$prediction == "1", "Yes", "No")

# confusion matrix
cm <- confusionMatrix(as.factor(testResults_svm$prediction), as.factor(testResults_svm$observation))
print(cm)
```

svmRadial

```
## Confusion Matrix and Statistics
##
```

```
##           Reference
## Prediction  No Yes
##        No  150   3
##        Yes  10   8
##
##                Accuracy : 0.924
##                  95% CI : (0.8735, 0.9589)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 0.78756
##
##                   Kappa : 0.5128
##
##  Mcnemar's Test P-Value : 0.09609
##
##             Sensitivity : 0.9375
##             Specificity : 0.7273
##          Pos Pred Value : 0.9804
##          Neg Pred Value : 0.4444
##              Prevalence : 0.9357
##          Detection Rate : 0.8772
##    Detection Prevalence : 0.8947
##       Balanced Accuracy : 0.8324
##
##        'Positive' Class : No
##
```

```
# svm Radial result plot
plot(svm_model)
```




```
svm_model$finalModel
```

```
## Support Vector Machine object of class "ksvm"
##
## SV type: C-svc  (classification)
##  parameter : cost C = 4
##
## Gaussian Radial Basis kernel function.
##  Hyperparameter : sigma =  0.0579991726665963
##
## Number of Support Vectors : 160
##
## Objective Function Value : -249.4782
## Training error : 0.024745
## Probability model included.
```

```
# roc/auc result
roc_svm <- roc(testResults_svm$observation, testResults_svm$class_prob)
```

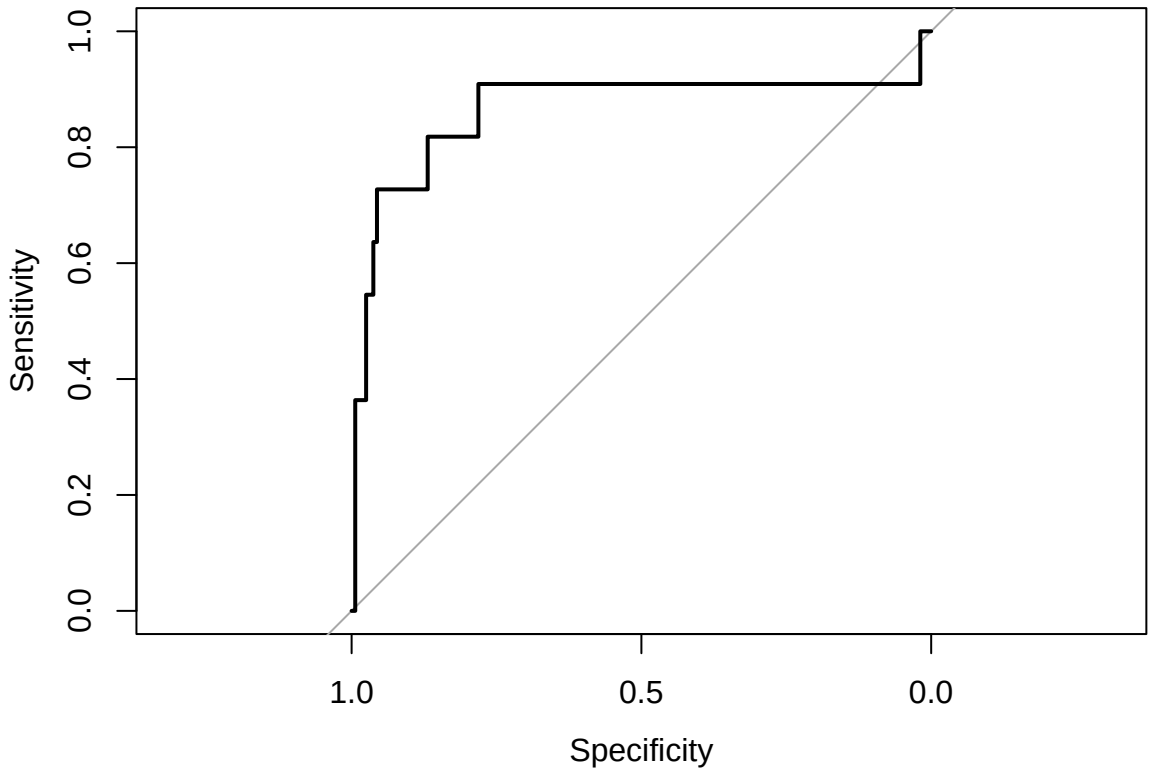
```
## Setting levels: control = No, case = Yes
```

```
## Setting direction: controls < cases
```

```
auc(roc_svm)
```

```
## Area under the curve: 0.8648
```

```
plot(roc_svm)
```



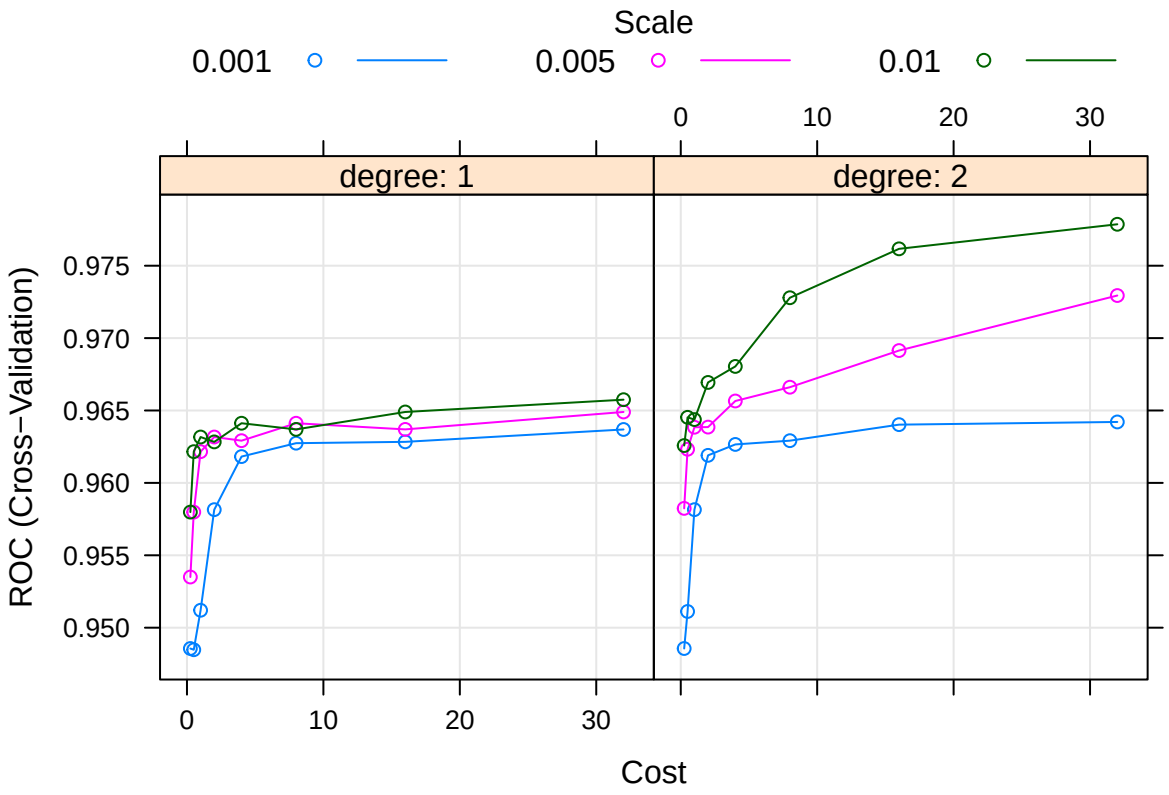

```
svm_modelPoly <- train_svm_poly(train_X, train_y, cntrl)
```

```
# get prediction result
testResults_svmP <- get_prediction_results(svm_modelPoly, test_X, test_y)

# convert prediction levels to match observation
testResults_svmP$prediction <- ifelse(testResults_svmP$prediction == "1", "Yes", "No")

# confusion matrix
cm <- confusionMatrix(as.factor(testResults_svmP$prediction), as.factor(testResults_svmP$observation))
print(cm)
```

svmPoly

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  152   3
##        Yes   8   8
##
##                Accuracy : 0.9357
##                  95% CI : (0.8878, 0.9675)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 0.5793
##
##                   Kappa : 0.559
##
##  Mcnemar's Test P-Value : 0.2278
##
##             Sensitivity : 0.9500
##             Specificity : 0.7273
##          Pos Pred Value : 0.9806
##          Neg Pred Value : 0.5000
##              Prevalence : 0.9357
##          Detection Rate : 0.8889
##    Detection Prevalence : 0.9064
##       Balanced Accuracy : 0.8386
##
##        'Positive' Class : No
##
```

```
# svm Poly result plot
plot(svm_modelPoly)
```




```
svm_modelPoly$finalModel
```

```
## Support Vector Machine object of class "ksvm"
##
## SV type: C-svc  (classification)
##  parameter : cost C = 32
##
## Polynomial kernel function.
##  Hyperparameters : degree =  2  scale =  0.01  offset =  1
##
## Number of Support Vectors : 107
##
## Objective Function Value : -2296.99
## Training error : 0.03639
## Probability model included.
```

```
# roc/auc result
roc_svmp <- roc(testResults_svmP$observation, testResults_svmP$class_prob)
```

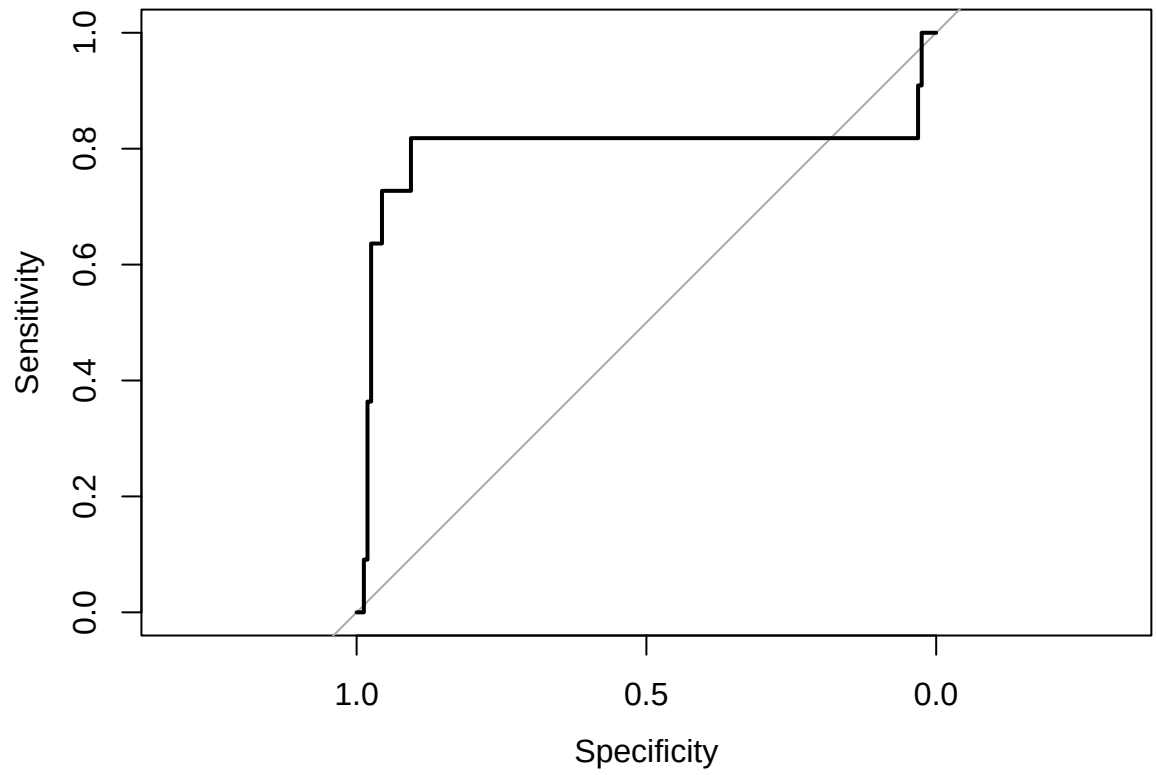
```
## Setting levels: control = No, case = Yes
```

```
## Setting direction: controls < cases
```

```
auc(roc_svmp)
```

```
## Area under the curve: 0.7977
```

```
plot(roc_svmp)
```



K-Nearest Neighbors

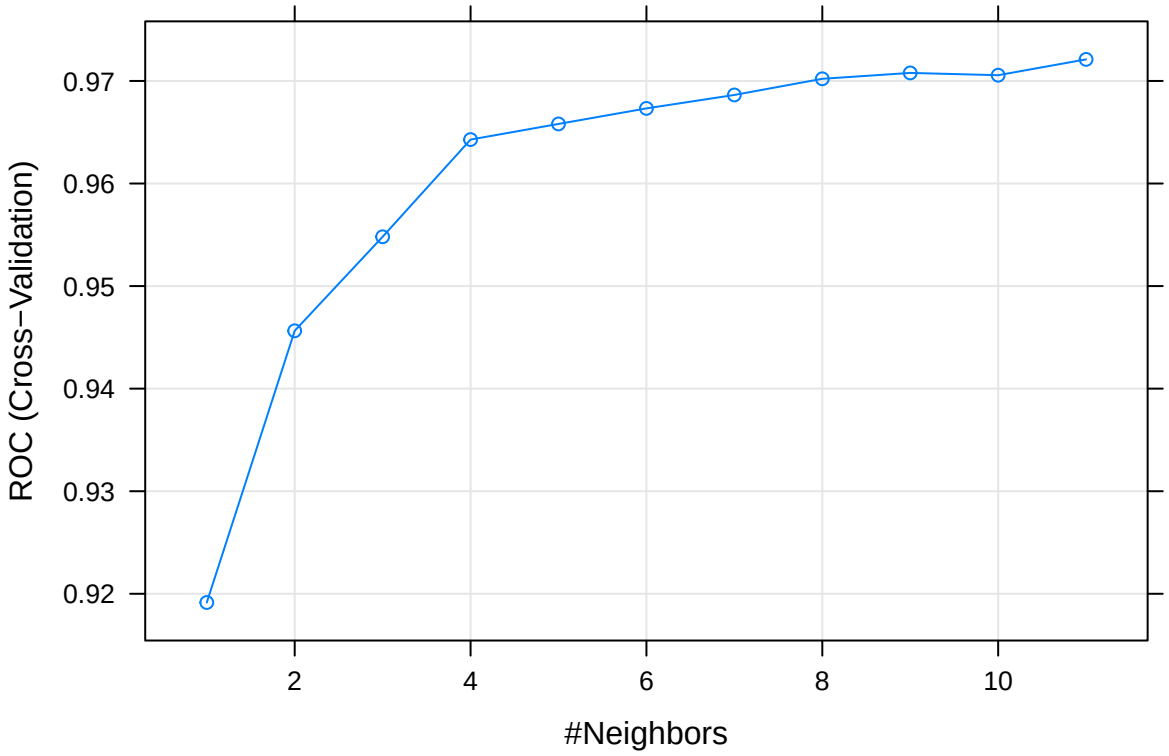
```
knn_model <- knn_model_train(train_X, train_y, cntrl, 1:11)
```

```
## Warning in train.default(x = train_X, y = train_y, method = "knn", tuneGrid =
## knnGrid, : The metric "Accuracy" was not in the result set. ROC will be used
## instead.
```

```
# get prediction result
testResults_knn <- get_prediction_results(knn_model, test_X, test_y)


# convert prediction levels to match observation
testResults_knn$prediction <- ifelse(testResults_knn$prediction == "1", "Yes", "No")

# confusion matrix
cm <- confusionMatrix(as.factor(testResults_knn$prediction), as.factor(testResults_knn$observation))
print(cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  150   3
##        Yes  10   8
##
##                Accuracy : 0.924
##                  95% CI : (0.8735, 0.9589)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 0.78756
##
##                   Kappa : 0.5128
##
##  Mcnemar's Test P-Value : 0.09609
##
##             Sensitivity : 0.9375
##             Specificity : 0.7273
##          Pos Pred Value : 0.9804
##          Neg Pred Value : 0.4444
##              Prevalence : 0.9357
##          Detection Rate : 0.8772
##    Detection Prevalence : 0.8947
##       Balanced Accuracy : 0.8324
##
##        'Positive' Class : No
##
```

```
# kNN result plot
plot(knn_model)
```




```
knn_model$finalModel
```

```
## 11-nearest neighbor model
## Training set outcome distribution:
##
##  No Yes
## 337 350
```

```
# roc/auc result
roc_knn <- roc(testResults_knn$observation, testResults_knn$class_prob)
```

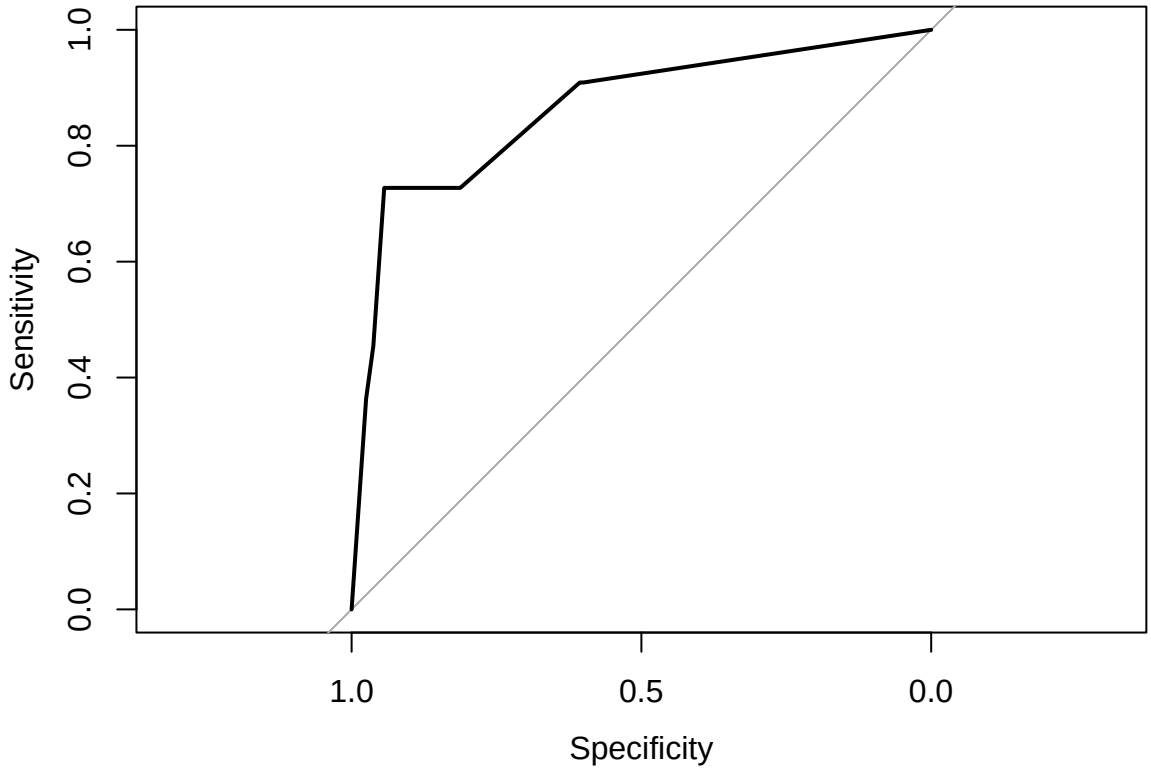
```
## Setting levels: control = No, case = Yes
```

```
## Setting direction: controls < cases
```

```
auc(roc_knn)
```

```
## Area under the curve: 0.8634
```

```
plot(roc_knn)
```



Random Forest Model

```
rf_model <- rf_model_train(train_X, train_y, cntrl)
```

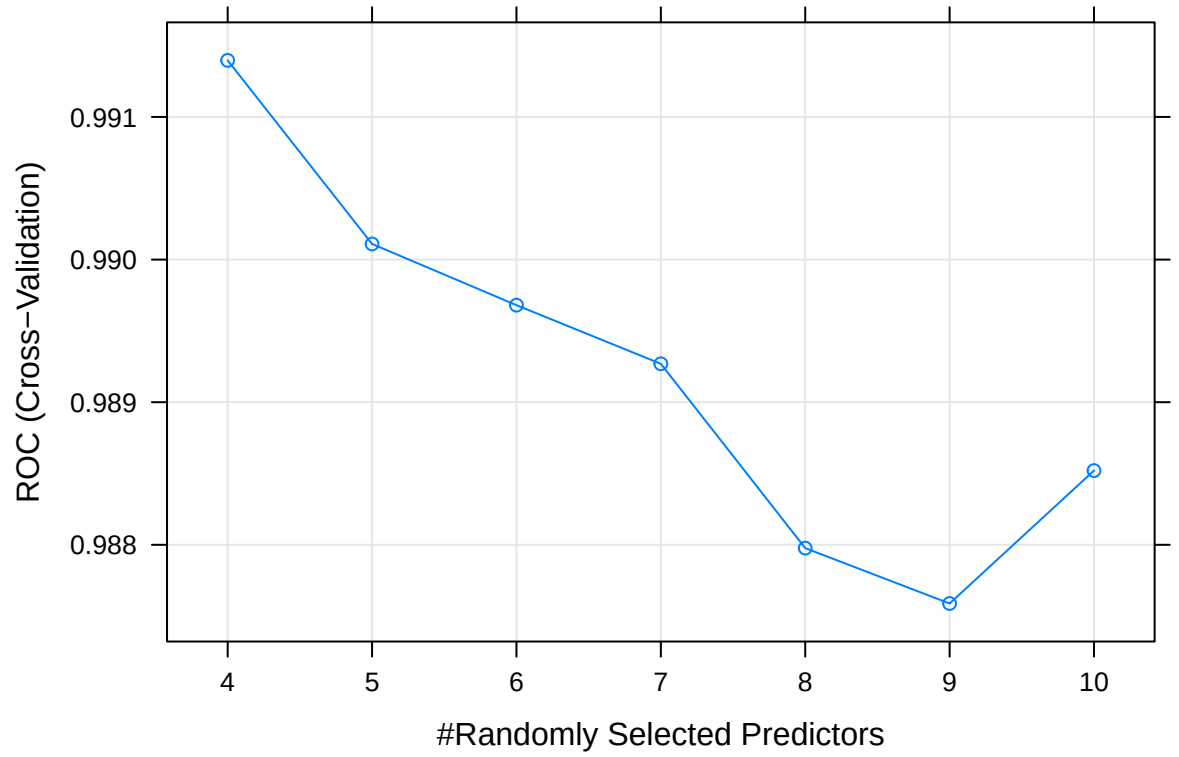
```
## Warning in train.default(x = train_X, y = train_y, method = "rf", tuneGrid =
## mtryGrid, : The metric "Accuracy" was not in the result set. ROC will be used
## instead.
```

```
# get prediction result
testResults_rf <- get_prediction_results(rf_model, test_X, test_y)

# convert prediction levels to match observation
testResults_rf$prediction <- ifelse(testResults_rf$prediction == "1", "Yes", "No")

# confusion matrix
cm <- confusionMatrix(as.factor(testResults_rf$prediction), as.factor(testResults_rf$observation))
print(cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  152   3
##        Yes   8   8
##
##                Accuracy : 0.9357
```

```
##                  95% CI : (0.8878, 0.9675)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 0.5793
##
##                   Kappa : 0.559
##
##  Mcnemar's Test P-Value : 0.2278
##
##             Sensitivity : 0.9500
##             Specificity : 0.7273
##          Pos Pred Value : 0.9806
##          Neg Pred Value : 0.5000
##              Prevalence : 0.9357
##          Detection Rate : 0.8889
##    Detection Prevalence : 0.9064
##       Balanced Accuracy : 0.8386
##
##        'Positive' Class : No
##
```

```
# RF result plot
plot(rf_model)
```




```
rf_model$finalModel
```

```
##
```

```
## Call:
##  randomForest(x = x, y = y, mtry = param$mtry, importance = TRUE)
##                Type of random forest: classification
##                      Number of trees: 500
## No. of variables tried at each split: 4
##
##         OOB estimate of  error rate: 4.95%
## Confusion matrix:
##      No Yes class.error
## No  327  10  0.02967359
## Yes  24 326  0.06857143
```

```
# roc/auc result
roc_rf <- roc(testResults_rf$observation, testResults_rf$class_prob)
```

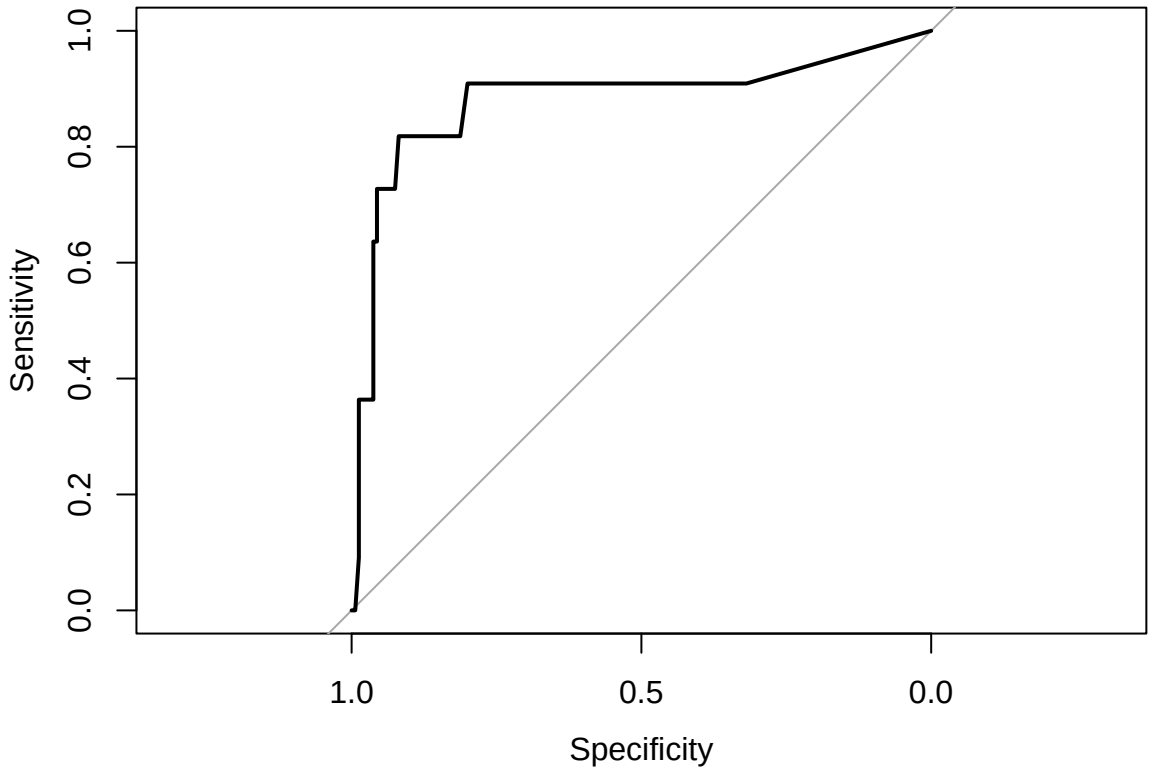
```
## Setting levels: control = No, case = Yes
```

```
## Setting direction: controls < cases
```

```
auc(roc_rf)
```

```
## Area under the curve: 0.8804
```

```
plot(roc_rf)
```



Linear Model

Logistic Regression

```
lr_model <- lr_model_train(train_X, train_y, cntrl)
```

```
# get prediction result
testResults_lr <- get_prediction_results(lr_model, test_X, test_y)


# convert prediction levels to match observation
testResults_lr$prediction <- ifelse(testResults_lr$prediction == "1", "Yes", "No")


# confusion matrix
cm <- confusionMatrix(as.factor(testResults_lr$prediction), as.factor(testResults_lr$observation))
print(cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  151   3
##        Yes   9   8
##
##                Accuracy : 0.9298
##                  95% CI : (0.8806, 0.9632)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 0.6924
##
##                   Kappa : 0.5351
##
##  Mcnemar's Test P-Value : 0.1489
##
##             Sensitivity : 0.9437
##             Specificity : 0.7273
##          Pos Pred Value : 0.9805
##          Neg Pred Value : 0.4706
##              Prevalence : 0.9357
##          Detection Rate : 0.8830
##    Detection Prevalence : 0.9006
##       Balanced Accuracy : 0.8355
##
##        'Positive' Class : No
##
```

```
# roc/auc result

roc_lr <- roc(testResults_lr$observation, testResults_lr$class_prob)
```

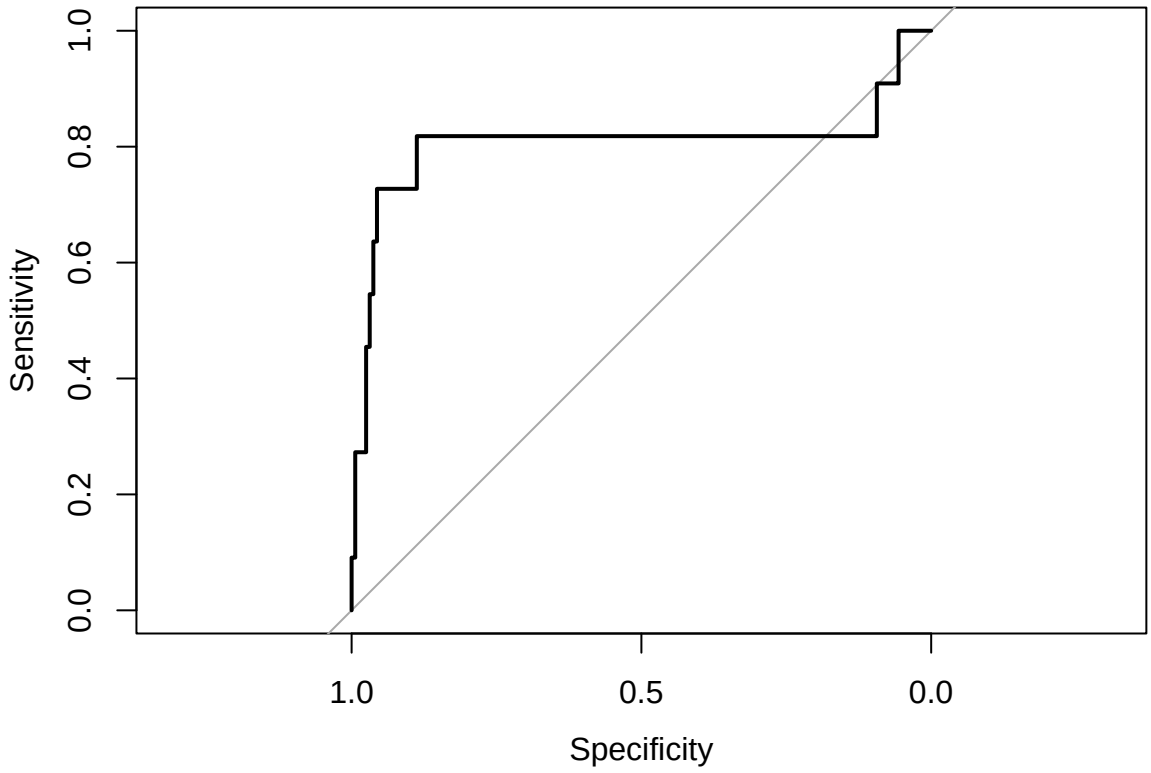
```
## Setting levels: control = No, case = Yes
```

```
## Setting direction: controls < cases
```

```
auc(roc_lr)
```

```
## Area under the curve: 0.8057
```

```
plot(roc_lr)
```



LDA Model

```
lda_model <- lda_model_train(train_X, train_y, cntrl)
```

```
# get prediction result
testResults_lda <- get_prediction_results(lda_model, test_X, test_y)

# convert prediction levels to match observation
testResults_lda$prediction <- ifelse(testResults_lda$prediction == "1", "Yes", "No")


# confusion matrix
cm <- confusionMatrix(as.factor(testResults_lda$prediction), as.factor(testResults_lda$observation))
print(cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  152   3
##        Yes   8   8
##
##                Accuracy : 0.9357
##                  95% CI : (0.8878, 0.9675)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 0.5793
##
##                   Kappa : 0.559
##
##  Mcnemar's Test P-Value : 0.2278
##
##             Sensitivity : 0.9500
##             Specificity : 0.7273
##          Pos Pred Value : 0.9806
##          Neg Pred Value : 0.5000
##              Prevalence : 0.9357
##          Detection Rate : 0.8889
##    Detection Prevalence : 0.9064
##       Balanced Accuracy : 0.8386
##
##        'Positive' Class : No
##
```

```
# roc/auc result
roc_lda <- roc(testResults_lda$observation, testResults_lda$class_prob)
```

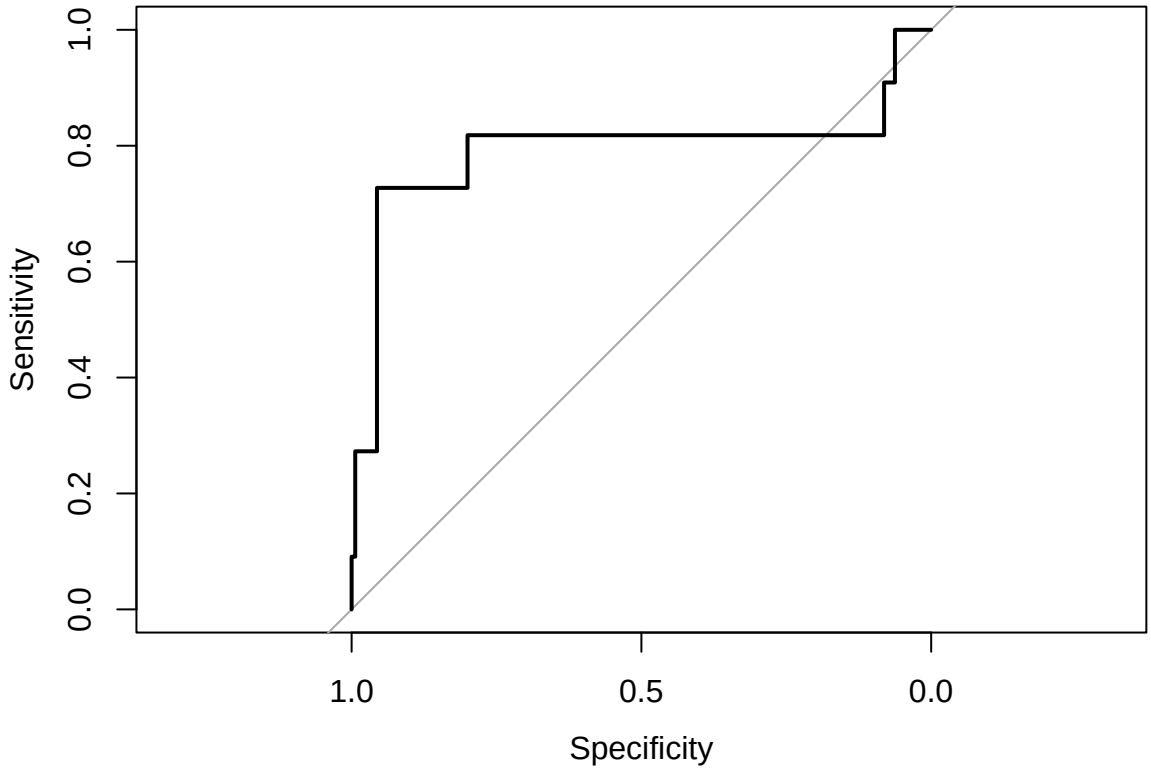
```
## Setting levels: control = No, case = Yes
```

```
## Setting direction: controls < cases
```

```
auc(roc_lda)
```

```
## Area under the curve: 0.792
```

```
plot(roc_lda)
```



Penalized Logistic Regression

```
glmn_model <- glmn_model_train(train_X, train_y, cntrl)
```

```
# get prediction result
testResults_glmn <- get_prediction_results(glmn_model, test_X, test_y)

# convert prediction levels to match observation
testResults_glmn$prediction <- ifelse(testResults_glmn$prediction == "1", "Yes", "No")

# confusion matrix
cm <- confusionMatrix(as.factor(testResults_glmn$prediction), as.factor(testResults_glmn$observation))
print(cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  152   3
##        Yes   8   8
##
##                Accuracy : 0.9357
##                  95% CI : (0.8878, 0.9675)
```

```
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 0.5793
##
##                   Kappa : 0.559
##
##  Mcnemar's Test P-Value : 0.2278
##
##             Sensitivity : 0.9500
##             Specificity : 0.7273
##          Pos Pred Value : 0.9806
##          Neg Pred Value : 0.5000
##              Prevalence : 0.9357
##          Detection Rate : 0.8889
##    Detection Prevalence : 0.9064
##       Balanced Accuracy : 0.8386
##
##        'Positive' Class : No
##
```

```
# roc/auc result
roc_glmn <- roc(testResults_glmn$observation, testResults_glmn$class_prob)
```

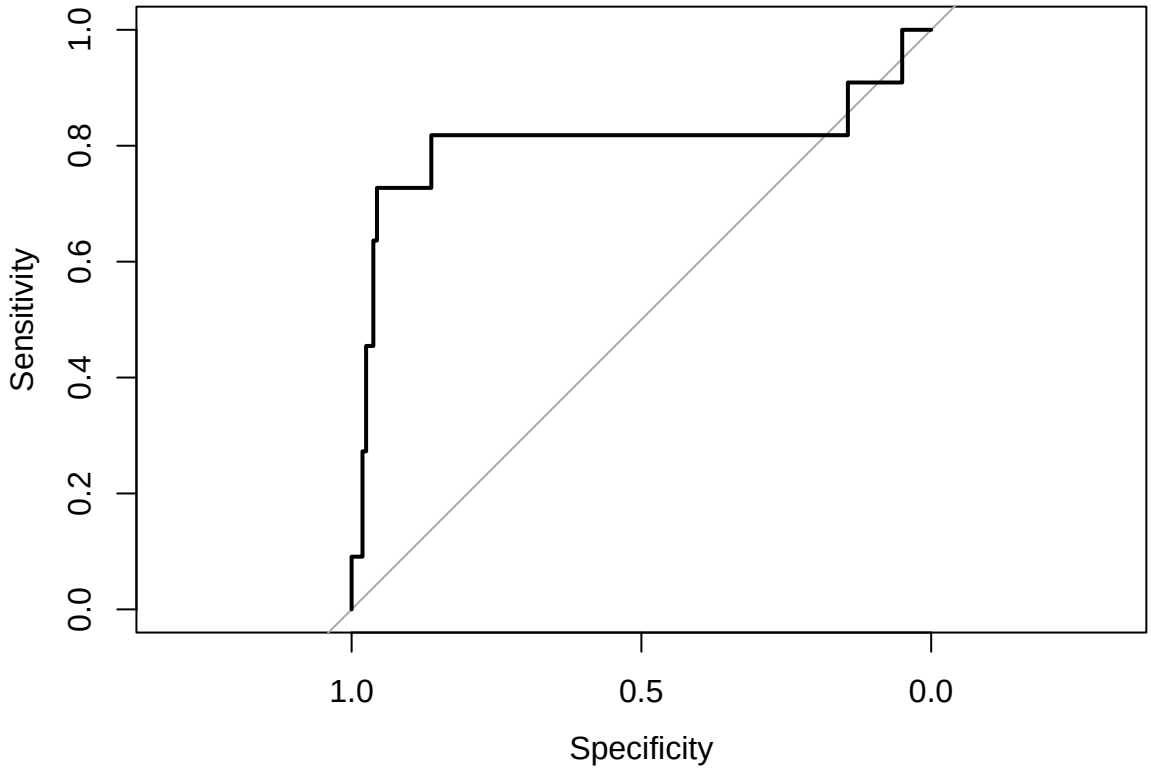
```
## Setting levels: control = No, case = Yes
```

```
## Setting direction: controls < cases
```

```
auc(roc_glmn)
```

```
## Area under the curve: 0.8045
```

```
plot(roc_glmn)
```



Nearest Shrunken Centroids

```
nsc_model <- nsc_model_train(train_X, train_y, cntrl)
```

```
## 11111111111
```

```
# get prediction result
testResults_nsc <- get_prediction_results(nsc_model, test_X, test_y)

# convert prediction levels to match observation
testResults_nsc$prediction <- ifelse(testResults_nsc$prediction == "1", "Yes", "No")


# confusion matrix
cm <- confusionMatrix(as.factor(testResults_nsc$prediction), as.factor(testResults_nsc$observation))
print(cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  152   3
##        Yes   8   8
```

```
##
##                Accuracy : 0.9357
##                  95% CI : (0.8878, 0.9675)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 0.5793
##
##                   Kappa : 0.559
##
##  Mcnemar's Test P-Value : 0.2278
##
##             Sensitivity : 0.9500
##             Specificity : 0.7273
##          Pos Pred Value : 0.9806
##          Neg Pred Value : 0.5000
##              Prevalence : 0.9357
##          Detection Rate : 0.8889
##    Detection Prevalence : 0.9064
##       Balanced Accuracy : 0.8386
##
##        'Positive' Class : No
##
```

```
# roc/auc result
roc_nsc <- roc(testResults_nsc$observation, testResults_nsc$class_prob)
```

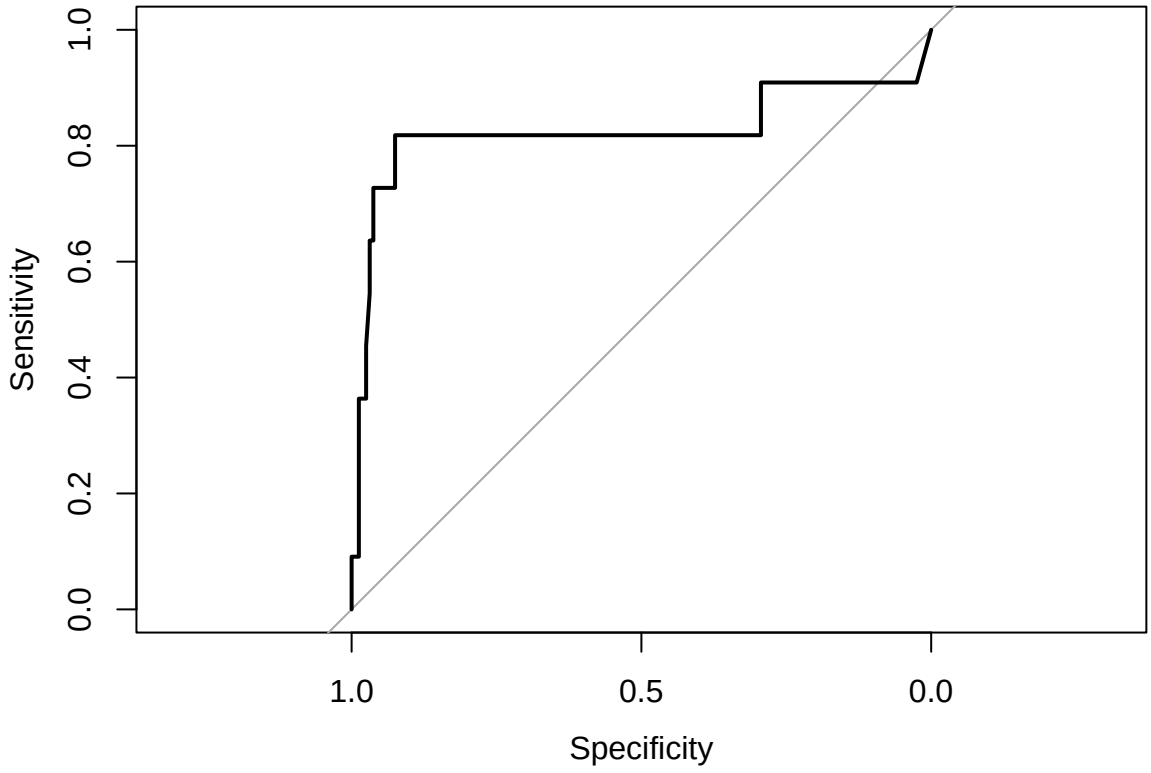
```
## Setting levels: control = No, case = Yes
```

```
## Setting direction: controls < cases
```

```
auc(roc_nsc)
```

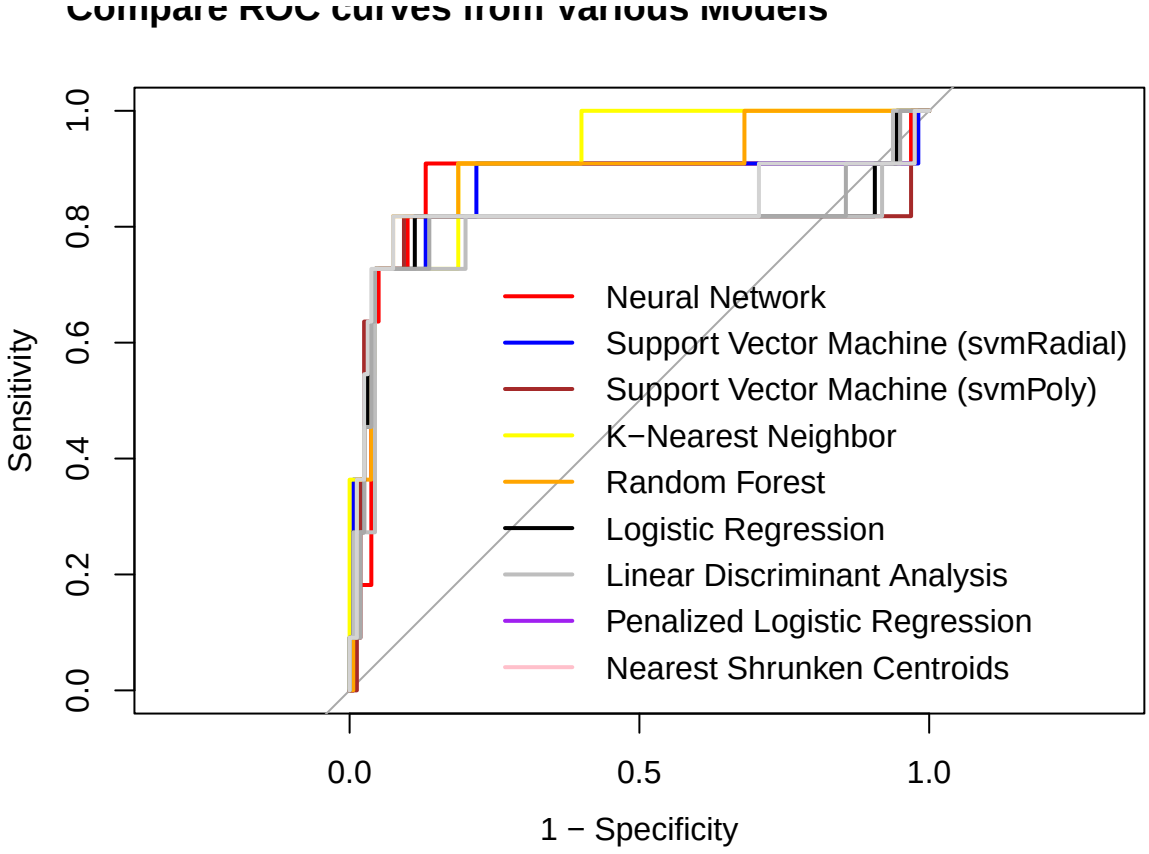
```
## Area under the curve: 0.8247
```

```
plot(roc_nsc)
```



Final Model Evaluation & Enhancements

```
### Compare Models using ROC curve
par(mar = c(9, 1, 0, 9))

# Non-linear model plots
plot(roc_nnet, type = "s", col = 'red', legacy.axes = TRUE)
plot(roc_svm, type = "s", add = TRUE, col = 'blue', legacy.axes = TRUE)
plot(roc_svmp, type = "s", add = TRUE, col = 'brown', legacy.axes = TRUE)
plot(roc_knn, type = "s", add = TRUE, col = 'yellow', legacy.axes = TRUE)
plot(roc_rf, type = "s", add = TRUE, col = 'orange', legacy.axes = TRUE)

# Linear model plots
plot(roc_lr, type = "s", add = TRUE, col = 'black', legacy.axes = TRUE)
plot(roc_lda, type = "s", add = TRUE, col = 'gray', legacy.axes = TRUE)
plot(roc_glmn, type = "s", add = TRUE, col = 'darkgray', legacy.axes = TRUE)
plot(roc_nsc, type = "s", add = TRUE, col = 'lightgray', legacy.axes = TRUE)

# Update the legend to include the new models
legend("bottomright", legend=c("Neural Network", "Support Vector Machine (svmRadial)", "Support Vector
       col=c("red", "blue", "brown", "yellow", "orange", "black", "gray", "purple", "pink"), lwd=2, bty

title(main = "Compare ROC curves from Various Models")
```



Model performance based on different metrics (AUC/ROC, Accuracy)

```
# auc result
nnetAuc <- auc(roc_nnet)
marsAuc <- auc(roc_mars)
svmAuc <- auc(roc_svm)
svmpAuc <- auc(roc_svmp)
knnAuc <- auc(roc_knn)
rfAuc <- auc(roc_rf)
lrAuc <- auc(roc_lr)
ldaAuc <- auc(roc_lda)
glmnAuc <- auc(roc_glmn)
nscAuc <- auc(roc_nsc)

# accuracy result
nnetAcc <- get_accuracy(nnet_model, test_X, test_y)
marsAcc <- get_accuracy(mars_model, test_X, test_y)
svmAcc <- get_accuracy(svm_model, test_X, test_y)
svmpAcc <- get_accuracy(svm_modelPoly, test_X, test_y)
knnAcc <- get_accuracy(knn_model, test_X, test_y)
rfAcc <- get_accuracy(rf_model, test_X, test_y)
lrAcc <- get_accuracy(lr_model, test_X, test_y)
ldaAcc <- get_accuracy(lda_model, test_X, test_y)
glmnAcc <- get_accuracy(glmn_model, test_X, test_y)
```

```r
nscAcc <- get_accuracy(nsc_model, test_X, test_y)

auc_df <- data.frame(
  Model = c("Neural Network", "MARS", "Support Vector Machine (svmRadial)", "Support Vector Machine (sv
                                "K-Nearest Neighbor", "Random Forest", "Logistic Regression", "Linear Di
                                 "Penalized Logistic Regression", "Nearest Shrunken Centroids"),

  AUC = c(nnetAuc, marsAuc, svmAuc, svmpAuc, knnAuc, rfAuc, lrAuc, ldaAuc, glmnAuc, nscAuc),
  Accuracy = c(nnetAcc, marsAcc, svmAcc, svmpAcc, knnAcc, rfAcc, lrAcc, ldaAcc, glmnAcc, nscAcc)
)

print(auc_df)
```

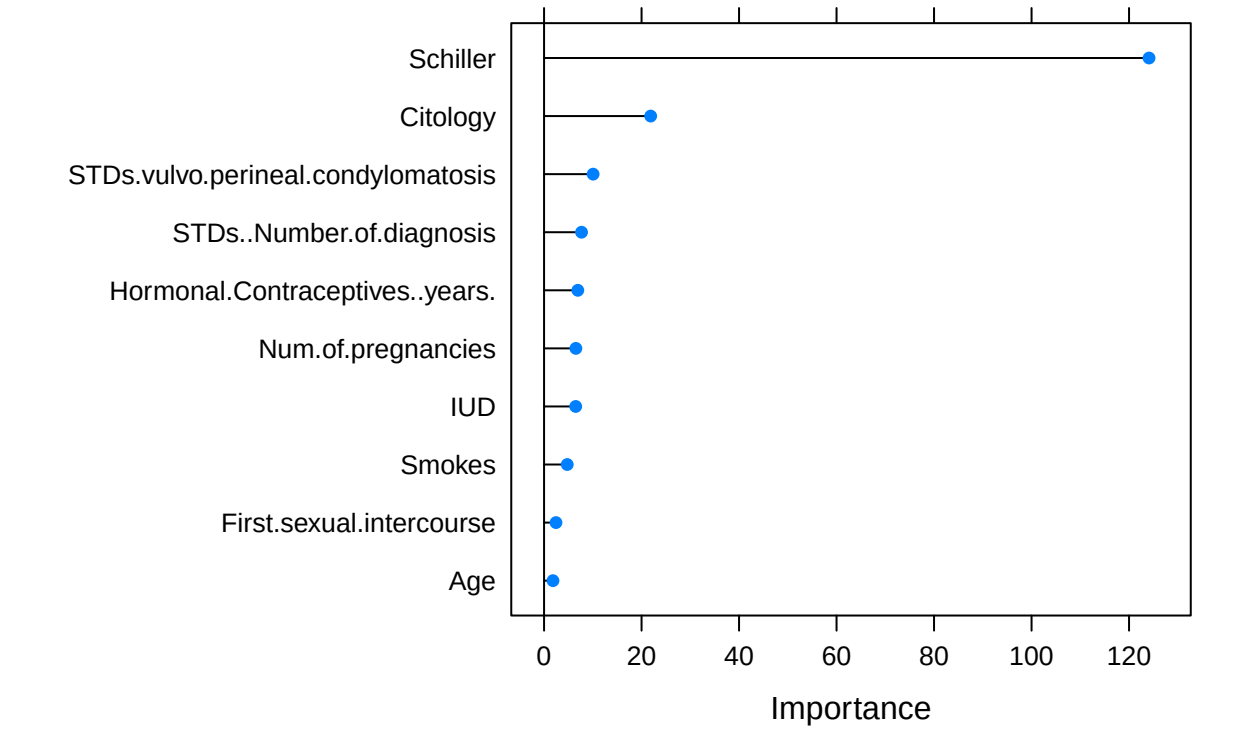
```
##                                Model       AUC  Accuracy
## 1                     Neural Network 0.8661932 0.9298246
## 2                               MARS 0.8389205 0.9298246
## 3  Support Vector Machine (svmRadial) 0.8647727 0.9239766
## 4    Support Vector Machine (svmPoly) 0.7977273 0.9356725
## 5                  K-Nearest Neighbor 0.8633523 0.9239766
## 6                       Random Forest 0.8803977 0.9356725
## 7                 Logistic Regression 0.8056818 0.9298246
## 8        Linear Discriminant Analysis 0.7920455 0.9356725
## 9       Penalized Logistic Regression 0.8045455 0.9356725
## 10         Nearest Shrunken Centroids 0.8247159 0.9356725
```

```r
# best model based on the AUC curve
best_model <- auc_df[which.max(auc_df$AUC), ]

print(best_model)
```

```
##           Model       AUC  Accuracy
## 6 Random Forest 0.8803977 0.9356725
```

Checking the important variables of the optimal model

```r
plot(varImp(rf_model, scale = FALSE), top = 10,
     main = "Important Factors for Predicting Cervical Cancer using Random Forest")
```



Recursive Feature Elimination (RFE)

```
# use caret package & user-defined-function in Modeling.R to do recursive feature elimination
optimal_rf_features <- rf_rfe(train_X, train_y)
print(optimal_rf_features)
```

```
##  [1] "Schiller"                          "Citology"
##  [3] "STDs.vulvo.perineal.condylomatosis" "Hormonal.Contraceptives..years."
##  [5] "Num.of.pregnancies"                "STDs..Number.of.diagnosis"
##  [7] "IUD"                               "Smokes"
##  [9] "First.sexual.intercourse"          "Number.of.sexual.partners"
## [11] "Age"
```

```
# Retrain penalized LR with optimal features - 12 out of 15
train_X_rfe <- train_X[, optimal_rf_features]

rf_model_rfe <- rf_model_train(train_X_rfe, train_y, cntrl)
rf_model_rfe
```

```
## Random Forest
##
## 687 samples
##  11 predictor
```

```
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 618, 618, 618, 618, 619, 619, ...
## Resampling results across tuning parameters:
##
##   mtry  ROC        Sens       Spec
##    3    0.9930125  0.9762923  0.9371429
##    4    0.9912618  0.9733512  0.9371429
##    5    0.9903196  0.9645276  0.9428571
##    6    0.9889419  0.9704100  0.9400000
##    7    0.9876802  0.9645276  0.9457143
##    8    0.9875465  0.9704100  0.9400000
##    9    0.9873848  0.9644385  0.9428571
##   10    0.9879730  0.9644385  0.9457143
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 3.
```

```
# Test new model
test_X_rfe <- test_X[, optimal_rf_features]

# get prediction result
testResults_rf_rfe <- get_prediction_results(rf_model_rfe, test_X_rfe, test_y)


testResults_rf_rfe$prediction <- ifelse(testResults_rf_rfe$prediction == "1", "Yes", "No")

# confusion matrix
cm <- confusionMatrix(as.factor(testResults_rf_rfe$prediction), as.factor(testResults_rf_rfe$observatio
print(cm)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  No Yes
##        No  152   3
##        Yes   8   8
##
##                Accuracy : 0.9357
##                  95% CI : (0.8878, 0.9675)
##     No Information Rate : 0.9357
##     P-Value [Acc > NIR] : 0.5793
##
##                   Kappa : 0.559
##
##  Mcnemar's Test P-Value : 0.2278
##
##             Sensitivity : 0.9500
##             Specificity : 0.7273
##          Pos Pred Value : 0.9806
##          Neg Pred Value : 0.5000
##              Prevalence : 0.9357
```

```
##          Detection Rate : 0.8889
##    Detection Prevalence : 0.9064
##       Balanced Accuracy : 0.8386
##
##        'Positive' Class : No
##
```

```
# roc/auc result
roc_rf_rfe <- roc(testResults_rf_rfe$observation, testResults_rf_rfe$class_prob)
```

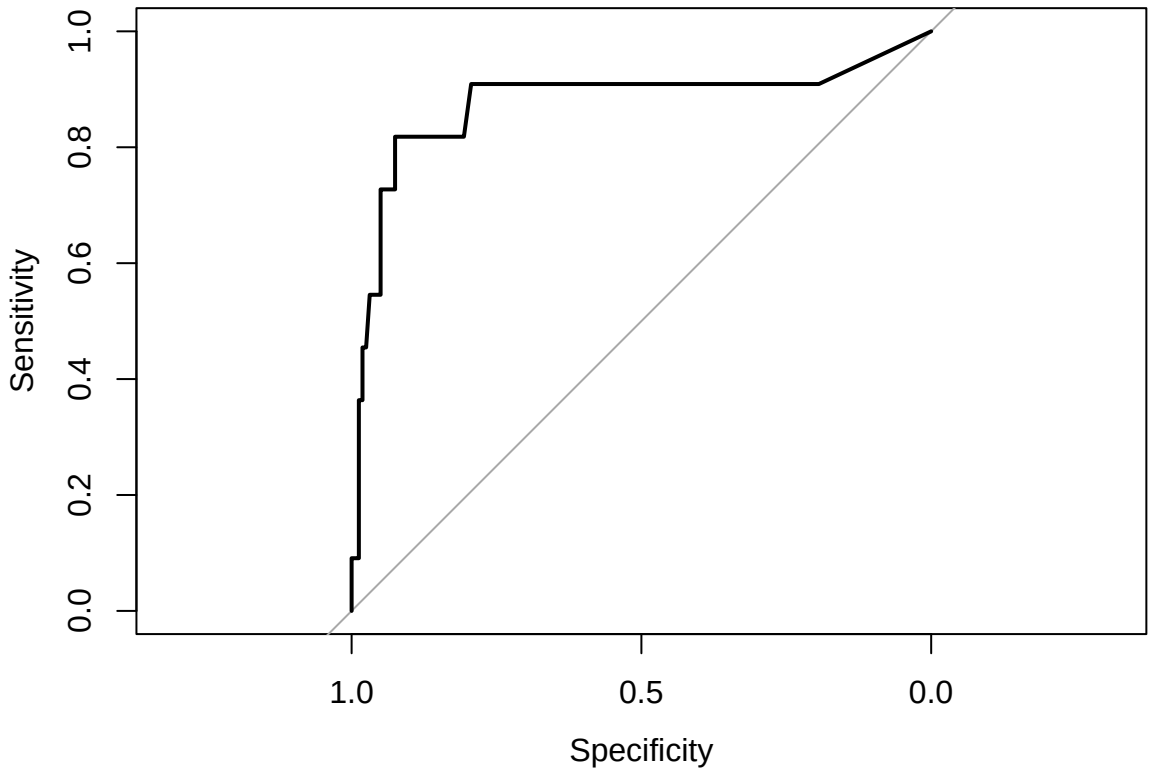
```
## Setting levels: control = No, case = Yes
```

```
## Setting direction: controls < cases
```

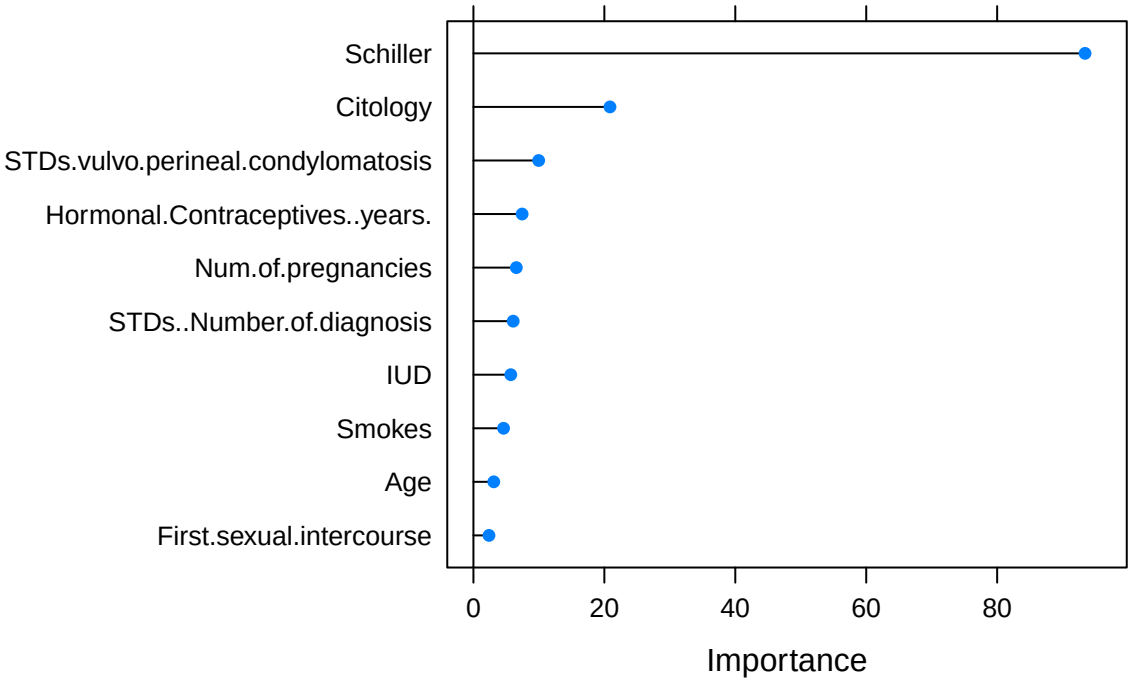
```
auc(roc_rf_rfe)
```

```
## Area under the curve: 0.8761
```

```
plot(roc_rf_rfe)
```




```
# var importance of final glmnet model
plot(varImp(rf_model_rfe, scale = FALSE), top = 10,
     main = "Important Factors for Predicting Cervical Cancer\n using Penalized Random Forest")
```



Threshold Investigation

```
threshold_df <- thresholds_cm(testResults_rf_rfe)
print(threshold_df)
```

```
##   Threshold TP FP  TN FN
## 1       0.1  9 20 140  2
## 2       0.2  9 15 145  2
## 3       0.3  8 12 148  3
## 4       0.4  8  8 152  3
## 5       0.5  8  8 152  3
## 6       0.6  8  8 152  3
## 7       0.7  8  8 152  3
## 8       0.8  8  8 152  3
## 9       0.9  6  6 154  5
```